

SCORE Search Results Details for Application 09869098 and Search Result us-09-869-098a- 1_copy_1634_2270.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 09869098 and Search Result us-09-869-098a-1_copy_1634_2270.rst.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 20:17:19 ; Search time 4150 Seconds
(without alignments)
8583.281 Million cell updates/sec

Title: US-09-869-098A-1_COPY_1634_2270
Perfect score: 637
Sequence: 1 acctgttgctgcagttctga.....cgcccggtcgtccgacgcg 637

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	458	71.9	558	9	DB045257	DB045257 DB045257
2	439	68.9	560	9	DB047138	DB047138 DB047138
3	406.4	63.8	559	9	DA890833	DA890833 DA890833
4	301	47.3	314	9	DB045802	DB045802 DB045802
5	296.4	46.5	427	2	BI222607	BI222607 602940387
6	107.4	16.9	534	9	DA359011	DA359011 DA359011
7	101	15.9	630	3	BP305626	BP305626 BP305626
8	95	14.9	346	9	DB194182	DB194182 DB194182
9	95	14.9	566	9	DA903915	DA903915 DA903915
10	94	14.8	574	9	DA821600	DA821600 DA821600
11	78	12.2	326	8	CR991281	CR991281 CR991281
12	77	12.1	1012	2	BM552598	BM552598 AGENCOURT
13	74.4	11.7	512	9	DA947305	DA947305 DA947305
14	74.4	11.7	512	9	DB194024	DB194024 DB194024
15	74.4	11.7	551	9	DA650717	DA650717 DA650717
16	74.4	11.7	551	9	DA948494	DA948494 DA948494
17	74.4	11.7	558	9	DB193975	DB193975 DB193975
18	74.4	11.7	563	9	DB212683	DB212683 DB212683
19	74.4	11.7	576	9	DA960668	DA960668 DA960668
20	69	10.8	551	9	DA611037	DA611037 DA611037
21	69	10.8	552	9	DA267193	DA267193 DA267193
22	69	10.8	569	3	BP266791	BP266791 BP266791
23	69	10.8	582	3	BP305299	BP305299 BP305299
24	69	10.8	582	3	BP366225	BP366225 BP366225
25	68.4	10.7	555	9	DA605644	DA605644 DA605644
26	68	10.7	483	2	BM147070	BM147070 TCAAP1Q10
27	68	10.7	519	9	DA604317	DA604317 DA604317
28	68	10.7	579	9	DB108414	DB108414 DB108414
29	68	10.7	820	2	BG756947	BG756947 602715447
30	68	10.7	887	2	BG755627	BG755627 602716131
31	67.2	10.5	1690	6	CR860955	CR860955 Pongo pyg
32	67	10.5	251	7	BE174858	BE174858 QV2-HT057
33	67	10.5	551	3	BP297893	BP297893 BP297893
34	67	10.5	559	9	DA947215	DA947215 DA947215
35	67	10.5	561	9	DB008728	DB008728 DB008728
36	67	10.5	574	3	BP276551	BP276551 BP276551
37	67	10.5	583	9	DB111013	DB111013 DB111013
38	66.6	10.5	1237	9	DN690375	DN690375 CGX70-B04
39	66	10.4	256	9	DB120492	DB120492 DB120492
40	66	10.4	261	9	DB118608	DB118608 DB118608
41	66	10.4	266	9	DA820961	DA820961 DA820961
42	66	10.4	313	7	BE246787	BE246787 TCBAP1E44
43	66	10.4	352	9	DA963269	DA963269 DA963269
44	66	10.4	366	9	DB190019	DB190019 DB190019
45	66	10.4	422	9	DA957387	DA957387 DA957387

ALIGNMENTS

RESULT 1

DB045257

LOCUS

DB045257

558 bp

mRNA

linear

EST 11-NOV-2005

DEFINITION DB045257 TESTI2 Homo sapiens cDNA clone TESTI2033446 5', mRNA sequence.

ACCESSION DB045257

VERSION DB045257.1 GI:82062586

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 558)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers

source 1. .558
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TESTI2033446"
/tissue_type="testis"
/clone_lib="TESTI2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 71.9%; Score 458; DB 9; Length 558;
Best Local Similarity 99.8%; Pred. No. 3.1e-95;
Matches 469; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 168 AAAAGAGGAAGTGCACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCTTGGC 227
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Db 1 AAAAGAGGAAGTGCACTTAAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCTTGGC 59

Qy 228 TGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATC 287
|||||

Db 60 TGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATC 119

Qy 288 CTCACAGAGGTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTG 347
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Db 120 CTCACAGAGGTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTG 179

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Qy      348 ACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAG 407
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Db      180 ACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAG 239

Qy      408 AAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGT 467
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 AAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGT 299

Qy      468 CTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCAGGCCCCACCCGGGGCC 527
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Qy      528 CCGCCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCT 587
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Db      360 CCGCCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCT 419

Qy      588 GCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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RESULT 2

DB047138

LOCUS DB047138 560 bp mRNA linear EST 11-NOV-2005

DEFINITION DB047138 TESTI2 Homo sapiens cDNA clone TESTI2035855 5', mRNA sequence.

ACCESSION DB047138

VERSION DB047138.1 GI:82130461

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 560)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers


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source          1. .560
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                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="TESTI2035855"
                 /tissue_type="testis"
                 /clone_lib="TESTI2"
                 /note="Vector: pME18SFL3"

ORIGIN

Query Match      68.9%; Score 439; DB 9; Length 560;
Best Local Similarity 99.6%; Pred. No. 7.6e-91;
Matches 450; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      186 AAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCTGGCTGGGAAGGCAAGAGGTGT 245
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Db      1 AAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCTGGCTGGGAAGGCAAGAGGTGT 59

Qy      246 GTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGC 305
          |||
Db      60 GTGACTGGACAAGACTTGTTCCTGNCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGC 119

Qy      306 CCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAA 365
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Db      120 CCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAA 179

Qy      366 GGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAGAAAGTCATGGAGAGAACC 425
          |||
Db      180 GGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAGAAAGTCATGGAGAGAACC 239

Qy      426 CTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGA 485
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Qy      486 GCTGGCAGGCCCCGCCCCGCCCCGAGGCCACCCGGGCCCCGCCCCGAGGCTTAAG 545
          |||
Db      300 GCTGGCAGGCCCCGCCCCGCCCCGAGGCCACCCGGGCCCCGCCCCGAGGCTTAAG 359

Qy      546 CCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTG 605
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Db      360 CCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTG 419

Qy      606 ACTGTCCACGCTCGCCCCGGCTCGTCCGACGCG 637
          |||
Db      420 ACTGTCCACGCTCGCCCCGGCTCGTCCGACGCG 451

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RESULT 3

DA890833

LOCUS DA890833 559 bp mRNA linear EST 10-NOV-2005

DEFINITION DA890833 RECTM2 Homo sapiens cDNA clone RECTM2000758 5', mRNA sequence.

ACCESSION DA890833

VERSION DA890833.1 GI:81452209

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 559)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers

source 1. .559
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RECTM2000758"
/tissue_type="rectum"
/clone_lib="RECTM2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 63.8%; Score 406.4; DB 9; Length 559;
Best Local Similarity 99.5%; Pred. No. 2.6e-83;
Matches 418; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 213 AGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTCTTCTGGCG 272
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Db 1 AGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTCTTCTGGCG 60

Qy 273 GTCAGTCTTGCCATCCTCACAGAGGTTGGC-GGCCCAGAGAGTGTGAGGCAGAGGCGGG 331
|||||

Db 61 GTCAGTCTTGCCATCCTCACAGAGGTTGGCAGGCCCGAGAGAGTGTGAGGCAGAGGCGGG 120

Qy 332 GAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCAC 391
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Db 121 GAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCAC 180

Qy 392 GGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAG 451
|||||

Db 181 GGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAG 240

Qy 452 GCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCCGCCCCGCA 511
|||||

Db 241 GCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCCGCCCCGCA 300

Qy 512 GGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCC 571
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Db      301 GGCCCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCC 360
Qy      572 ACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCC 631
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Db      361 ACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTTC 420
  
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RESULT 4

DB045802

LOCUS DB045802 314 bp mRNA linear EST 11-NOV-2005

DEFINITION DB045802 TESTI2 Homo sapiens cDNA clone TESTI2034168 5', mRNA sequence.

ACCESSION DB045802

VERSION DB045802.1 GI:82069361

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 314)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers

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source      1. .314
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              /mol_type="mRNA"
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              /clone="TESTI2034168"
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              /note="Vector: pME18SFL3"
  
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ORIGIN

Query Match 47.3%; Score 301; DB 9; Length 314;

Best Local Similarity 99.4%; Pred. No. 5.9e-59;

Matches 312; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      213 AGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTCCTGGCG 272
  
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Db      1 AGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTCTGGCG 60
Qy      273 GTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGG 332
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Db      61 GTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGG 120
Qy      333 AGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACG 392
      |||
Db      121 AGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACG 180
Qy      393 GAAACG-GGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAG 451
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Db      181 GAAACGTGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAG 240
Qy      452 GCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCA 511
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Db      241 GCGGCTGCTCCAGGGTCTNCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCA 300
Qy      512 GGCCCCACCCCGGG 525
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Db      301 GGCCCCACCCCGGG 314

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RESULT 5

BI222607

LOCUS BI222607 427 bp mRNA linear EST 11-JUL-2001

DEFINITION 602940387F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103573 5', mRNA sequence.

ACCESSION BI222607

VERSION BI222607.1 GI:14676051

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 427)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11249 row: n column: 22

High quality sequence stop: 348.

FEATURES Location/Qualifiers

source 1..427

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5103573"

/tissue_type="cervical carcinoma cell line"

/lab_host="DH10B"

/clone_lib="NIH_MGC_12"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN

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Query Match          46.5%;   Score 296.4;   DB 2;   Length 427;
Best Local Similarity 93.0%;   Pred. No. 6.8e-58;
Matches 333; Conservative 0; Mismatches 21; Indels 4; Gaps 2;

Qy      152 GGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGT 211
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Db      1   GGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGTGACGCTGT 60

Qy      212 TAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTCCTGGC 271
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Db      61 AAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTCCTGGC 120

Qy      272 GGTCACTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGG 331
          |||
Db      121 GGTCACTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGG 180

Qy      332 GAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCAC 391
          |||
Db      181 GAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCAC 240

Qy      392 GGAAACGGGAGTGGAGAAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCG--CGGAA 449
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Db      241 GGAAACGGGAGTGGAGAAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGACGGAAA 300

Qy      450 AGGCGGCTGCTCCA--GGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGGCCCCGC 505
          |||
Db      301 GTGCGGCTGCTCCATGGGTCTCTGCACCCAAGTAGGAGCTGGCAGGCCACGTGCCAC 358

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RESULT 6

DA359011

LOCUS DA359011 534 bp mRNA linear EST 06-NOV-2005

DEFINITION DA359011 BRSTN2 Homo sapiens cDNA clone BRSTN2004725 5', mRNA
sequence.

ACCESSION DA359011

VERSION DA359011.1 GI:80897832

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 534)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai

FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES Location/Qualifiers
 source 1. .534
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="BRSTN2004725"
 /tissue_type="subthalamic nucleus"
 /clone_lib="BRSTN2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 16.9%; Score 107.4; DB 9; Length 534;
 Best Local Similarity 98.3%; Pred. No. 3.3e-14;
 Matches 119; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      518  ACCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCCCTGCGCGGAGCCCCACTGCG 577
          |||
Db      1  ACCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCCCTGCGCGGAGCCCCACTGCG 60

Qy      578  AAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGC-TCGCCCCGGCTCGTCCGACGC 636
          |||
Db      61  AAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCCTTCGCCTGGCTCGTCCGACGC 120

Qy      637  G 637
          |
Db      121  G 121
  
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RESULT 7

BP305626
 LOCUS BP305626 630 bp mRNA linear EST 17-SEP-2004
 DEFINITION BP305626 Sugano cDNA library, macrophage Homo sapiens cDNA clone
 MPG05177, mRNA sequence.
 ACCESSION BP305626
 VERSION BP305626.1 GI:52234586
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 630)
 AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki

Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Tel: 81-3-5449-5343
 Fax: 81-3-5449-5416
 Email: ysuzuki@hgc.jp.

FEATURES
 source Location/Qualifiers
 1. .630
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MPG05177"
 /cell_type="macrophage"
 /clone_lib="Sugano cDNA library, macrophage"

ORIGIN

Query Match 15.9%; Score 101; DB 3; Length 630;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 537 AGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCC 596
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 AGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCC 60

Qy 597 TTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
 ||||||||||||||||||||||||||||||||||||
 Db 61 TTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 101

RESULT 8

DB194182

LOCUS DB194182 346 bp mRNA linear EST 03-DEC-2005

DEFINITION DB194182 TOVAR2 Homo sapiens cDNA clone TOVAR2002676 5', mRNA sequence.

ACCESSION DB194182

VERSION DB194182.1 GI:83152118

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 346)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES
 source Location/Qualifiers
 1. .346
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TOVAR2002676"
 /tissue_type="ovary, tumor tissue"
 /clone_lib="TOVAR2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 14.9%; Score 95; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 543 AAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGA 602
 |||
 Db 1 AAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGA 60
 Qy 603 TTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
 |||
 Db 61 TTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 95

RESULT 9

DA903915

LOCUS DA903915 566 bp mRNA linear EST 13-NOV-2005

DEFINITION DA903915 SKNMC2 Homo sapiens cDNA clone SKNMC2004170 5', mRNA sequence.

ACCESSION DA903915

VERSION DA903915.1 GI:82359745

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 566)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

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JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai

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Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES
 source Location/Qualifiers
 1. .566
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SKNMC2004170"
 /cell_type="neuroepithelioma"
 /cell_line="SK-N-MC"
 /clone_lib="SKNMC2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 14.9%; Score 95; DB 9; Length 566;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 543 AAGCCGCGCCGCCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGA 602
 |||
 Db 1 AAGCCGCGCCGCCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGA 60
 Qy 603 TTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
 |||
 Db 61 TTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 95

RESULT 10

DA821600
 LOCUS DA821600 574 bp mRNA linear EST 11-NOV-2005
 DEFINITION DA821600 PERIC2 Homo sapiens cDNA clone PERIC2001607 5', mRNA sequence.
 ACCESSION DA821600
 VERSION DA821600.1 GI:82109269
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 574)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

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FEATURES                      Location/Qualifiers
    source                      1. .574
                                /organism="Homo sapiens"
                                /mol_type="mRNA"
                                /db_xref="taxon:9606"
                                /clone="PERIC2001607"
                                /tissue_type="pericardium"
                                /clone_lib="PERIC2"
                                /note="Vector: pME18SFL3"
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ORIGIN

Query Match 14.8%; Score 94; DB 9; Length 574;

Best Local Similarity 100.0%; Pred. No. 4.1e-11;

Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      544 AGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGAT 603
          |||
Db      1  AGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGAT 60
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Qy      604 TGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      61 TGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 94
```

RESULT 11

CR991281

LOCUS CR991281 326 bp mRNA linear EST 28-JUN-2005

DEFINITION CR991281 RZPD no.9017 Homo sapiens cDNA clone RZPDp9017D208 5', mRNA sequence.

ACCESSION CR991281

VERSION CR991281.1 GI:68285166

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 326)

AUTHORS Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.

TITLE Human T-Lymphocytes library

JOURNAL Unpublished (2005)

COMMENT Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD; RZPDp9017D208.

RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9017

http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available from RZPD;
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9017D208>
 contact RZPD (product-support@rzpd.de) for further information.
 Primer name: qe3_4 , Primer sequence: CGGATAACAATTCACACAG.

FEATURES
 source Location/Qualifiers
 1. .326
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="RZPDp9017D208"
 /tissue_type="T-Lymphocytes"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RZPD no.9017"
 /note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
 NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
 ; 1st strand cDNA was prepared from mRNA obtained from
 human T-Lymphocytes with a NotI - oligo(dT) primer [5'
 GACTAGTTCTAGATCGCGAGCGGCCGCTTTTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to SalI adaptors,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE80LSN_cloned vector"

ORIGIN

Query Match 12.2%; Score 78; DB 8; Length 326;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 560 GCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCG 619
 |||
 Db 1 GCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCG 60
 Qy 620 CCCGGCTCGTCCGACGCG 637
 |||
 Db 61 CCCGGCTCGTCCGACGCG 78

RESULT 12

BM552598

LOCUS BM552598 1012 bp mRNA linear EST 20-FEB-2002

DEFINITION AGENCOURT_6543723 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5549778
 5', mRNA sequence.

ACCESSION BM552598

VERSION BM552598.1 GI:18790596

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 1012)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12260 row: n column: 19
 High quality sequence stop: 524.

FEATURES
 source Location/Qualifiers
 1. .1012
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5549778"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb. "

ORIGIN

Query Match 12.1%; Score 77; DB 2; Length 1012;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 561 CGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGC 620
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 Db 1 CGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGC 60

 Qy 621 CCGGCTCGTCCGACGCG 637
 ||||||||||||||||
 Db 61 CCGGCTCGTCCGACGCG 77

RESULT 13

DA947305

LOCUS DA947305 512 bp mRNA linear EST 08-NOV-2005

DEFINITION DA947305 SPLEN2 Homo sapiens cDNA clone SPLEN2023327 5', mRNA
sequence.

ACCESSION DA947305

VERSION DA947305.1 GI:81200519

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 512)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

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 Identification and Characterization of Putative Alternative
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COMMENT Contact: Takao Isogai

FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES Location/Qualifiers
 source 1. .512
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SPLEN2023327"
 /tissue_type="spleen"
 /clone_lib="SPLEN2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 11.7%; Score 74.4; DB 9; Length 512;
 Best Local Similarity 98.7%; Pred. No. 1.4e-06;
 Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 621
 ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4 GCGAAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 63

 QY 622 CGGCTCGTCCGACGCG 637
 ||||||||||||||||
 Db 64 CGGCTCGTCCGACGCG 79

RESULT 14

DB194024
 LOCUS DB194024 512 bp mRNA linear EST 03-DEC-2005
 DEFINITION DB194024 TOVAR2 Homo sapiens cDNA clone TOVAR2002496 5', mRNA
 sequence.
 ACCESSION DB194024
 VERSION DB194024.1 GI:83151096
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
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COMMENT Contact: Takao Isogai
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 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES Location/Qualifiers
 source 1. .512
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TOVAR2002496"
 /tissue_type="ovary, tumor tissue"
 /clone_lib="TOVAR2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 11.7%; Score 74.4; DB 9; Length 512;
 Best Local Similarity 98.7%; Pred. No. 1.4e-06;
 Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 562 GCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 621
 ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4 GCGAAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 63

 Qy 622 CGGCTCGTCCGACGCG 637
 ||||||||||||||||
 Db 64 CGGCTCGTCCGACGCG 79

RESULT 15

DA650717
 LOCUS DA650717 551 bp mRNA linear EST 07-NOV-2005
 DEFINITION DA650717 MESAN2 Homo sapiens cDNA clone MESAN2004345 5', mRNA
 sequence.
 ACCESSION DA650717
 VERSION DA650717.1 GI:81137089
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 551)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MESAN2004345"
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 /clone_lib="MESAN2"
 /note="Vector: pME18SFL3; primary culture, normal mesangial cells"

ORIGIN

Query Match 11.7%; Score 74.4; DB 9; Length 551;
 Best Local Similarity 98.7%; Pred. No. 1.4e-06;
 Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      562 GCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 621
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Db      4   GCGAAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCC 63

Qy      622 CGGCTCGTCCGACGCG 637
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Db      64  CGGCTCGTCCGACGCG 79
  
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Search completed: June 6, 2006, 22:34:03
 Job time : 4154 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09869098 and Search Result us-09-869-098a- 1_copy_1634_2270.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09869098 and Search Result us-09-869-098a-1_copy_1634_2270.rnpbn.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 22:23:01 ; Search time 25 Seconds
(without alignments)
3000.881 Million cell updates/sec

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Perfect score: 637
Sequence: 1 acctgttgctgcagttctga.....cgcccggctcgtccgacgcg 637

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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c 1	41.8	6.6	1214	6	US-10-953-349-30760	Sequence 30760, A
c 2	41.8	6.6	4563	6	US-10-196-749-311	Sequence 311, App
c 3	41	6.4	3219	7	US-11-293-697-1221	Sequence 1221, Ap
c 4	40.8	6.4	2050	6	US-10-953-349-31154	Sequence 31154, A
c 5	40.4	6.3	2684	6	US-10-199-229-7	Sequence 7, Appli
c 6	39.8	6.2	1400	6	US-10-953-349-28773	Sequence 28773, A
c 7	38.8	6.1	42999	7	US-11-284-877-17	Sequence 17, Appl
c 8	38	6.0	1339	6	US-10-505-928-53	Sequence 53, Appl
c 9	38	6.0	2715	7	US-11-293-697-1028	Sequence 1028, Ap
c 10	37.8	5.9	461	6	US-10-953-349-30799	Sequence 30799, A
c 11	37.6	5.9	706	6	US-10-953-349-31527	Sequence 31527, A
c 12	37.4	5.9	461	6	US-10-953-349-30799	Sequence 30799, A
c 13	37.4	5.9	1073	6	US-10-953-349-37736	Sequence 37736, A
c 14	37.4	5.9	1354	7	US-11-293-697-208	Sequence 208, App
c 15	37.4	5.9	5703	7	US-11-312-958-63	Sequence 63, Appl
c 16	37.2	5.8	955	6	US-10-953-349-33699	Sequence 33699, A
c 17	37	5.8	1024	6	US-10-953-349-33192	Sequence 33192, A
c 18	36.6	5.7	1114	6	US-10-953-349-32119	Sequence 32119, A
c 19	36.4	5.7	1569	6	US-10-953-349-33558	Sequence 33558, A
c 20	36.4	5.7	1958	6	US-10-953-349-38532	Sequence 38532, A
c 21	36	5.7	2213	6	US-10-953-349-27640	Sequence 27640, A
c 22	36	5.7	3020	7	US-11-293-697-645	Sequence 645, App
c 23	36	5.7	38187	6	US-10-857-260-31	Sequence 31, Appl
c 24	35.8	5.6	2995	7	US-11-315-777-7	Sequence 7, Appli
c 25	35.6	5.6	706	6	US-10-953-349-31527	Sequence 31527, A
c 26	35.4	5.6	1540	6	US-10-953-349-29034	Sequence 29034, A
c 27	35.2	5.5	1587	7	US-11-293-697-136	Sequence 136, App
c 28	35.2	5.5	1822	6	US-10-505-928-16	Sequence 16, Appl
c 29	35.2	5.5	2134	6	US-10-196-749-369	Sequence 369, App
c 30	35.2	5.5	2267	7	US-11-293-697-2354	Sequence 2354, Ap
c 31	35.2	5.5	4763	6	US-10-505-928-374	Sequence 374, App
c 32	35	5.5	1122	6	US-10-953-349-31251	Sequence 31251, A
c 33	35	5.5	1357	6	US-10-953-349-34605	Sequence 34605, A
c 34	35	5.5	1667	6	US-10-505-928-419	Sequence 419, App
c 35	34.6	5.4	907	6	US-10-953-349-15391	Sequence 15391, A
c 36	34.6	5.4	1533	6	US-10-953-349-31890	Sequence 31890, A
c 37	34.6	5.4	1727	7	US-11-293-697-1686	Sequence 1686, Ap
c 38	34.6	5.4	1841	6	US-10-953-349-34354	Sequence 34354, A
c 39	34.4	5.4	626	6	US-10-953-349-39430	Sequence 39430, A
c 40	34.4	5.4	825	6	US-10-953-349-39057	Sequence 39057, A
c 41	34.4	5.4	1170	6	US-10-953-349-32139	Sequence 32139, A
c 42	34.4	5.4	1337	6	US-10-953-349-35245	Sequence 35245, A
c 43	34.4	5.4	1374	6	US-10-953-349-31642	Sequence 31642, A
c 44	34.4	5.4	1466	6	US-10-505-928-458	Sequence 458, App
c 45	34.4	5.4	2151	7	US-11-245-628-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-10-953-349-30760

; Sequence 30760, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30760
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-30760
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Best Local Similarity 56.0%; Pred. No. 0.15;
Matches 79; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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Qy      576 CGAAGCCCAGCTGCGCGCGCC 596
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Db      441 ATCGGACCTGCCAGGCGAGGC 461
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RESULT 2

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US-10-196-749-311/c
; Sequence 311, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
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; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 311
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-196-749-311
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Best Local Similarity 55.0%; Pred. No. 0.2;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
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Db      461 CCGCCGCGCCGCGCCGCGCCGCGCCGCGCAGGCTCCGCGCGCCCTCAGCCCGCTGCCCCCGCCC 402

Qy      484 GAGCTGGCAGGCCCCGGCCCCGCCCCGCGAGGCCCCACCCGGGCCCCCGCCCCCGAGGCTTA 543
      | ||| ||||| || || |||| | ||| ||||| ||||| ||| ||
Db      401 ACGGAGGCCAGCCCGCCCTAGCGCCGCGAGGCCCGGCCCCGGGCGAGCGCCGCGCCGCGCCGC 342

Qy      544 AGCCGCGCCGCGCCCTGCGCGGAGCCCCA 572
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Db      341 GGGCCCGCCGCGCCCATCGCGGCCCCCGA 313
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RESULT 3

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US-11-293-697-1221
; Sequence 1221, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1221
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1221
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Best Local Similarity 52.0%; Pred. No. 0.28;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
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Db      168 CAGGCAGGAGACTGGAGACGAGGTCTTGCAGGCGGAACTCAGGATGCTCTGAGCTGCCCCG 227

Qy      473 CACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCCGCC 532
      || | || | || | || | || | || | || | || | || | || |
Db      228 CACAACCCCTGGACCTTCACCCCTCGCCCCCTTCCCCGCATCCAGCTGCCCCAGCCCCCTGC 287

Qy      533 CCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGC 589
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RESULT 4

US-10-953-349-31154/c

; Sequence 31154, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 31154

; LENGTH: 2050

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-10-953-349-31154

Query Match 6.4%; Score 40.8; DB 6; Length 2050;

Best Local Similarity 50.5%; Pred. No. 0.28;

Matches 99; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Qy      435 GCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGG 494
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Db      1586 GCGGCACCAGCCAGAACGCCGACATGCCGGCGCCGCCGCCGCGCCAGCTCCAGCCTGC 1527

Qy      495 CCCGGCCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGC 554
      || | || | || | || | || | || | || | || | || | || |
Db      1526 GCCGCGCGCCCTCCACCGCGCCGACACGGCCATCGCCGCGGTGGCCAGCAGCAGGCCCA 1467

Qy      555 CGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCAC 614
      || | || | || | || | || | || | || | || | || | || |
Db      1466 CGCCGACGCGCTGCTTCATGGTGAGCCCCGCGGGTCGCCCCGTCACCCGTCGCAGCGCCG 1407

Qy      615 GCTCGCCCGGCTCGTC 630
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Db      1406 GCGCGATCCACCTGTC 1391

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RESULT 5

US-10-199-229-7/c

; Sequence 7, Application US/10199229

; Publication No. US20060099701A1

; GENERAL INFORMATION:

; APPLICANT: She, Jin-Xiong

; APPLICANT: Kumar, Pradeep

; APPLICANT: Wang, Cong-Yi

; TITLE OF INVENTION: ACTIVATORS OF CYCLIN-DEPENDENT KINASES

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; FILE REFERENCE: 5853-210
; CURRENT APPLICATION NUMBER: US/10/199,229
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2684
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-199-229-7
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Best Local Similarity 54.8%; Pred. No. 0.37;
Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
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Qy      456 CTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCAGGCC 515
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Db      458 CGGCTCCACGCGCACCGCCAGCAGCGCGGAGCGCGGTGGCCGGCCTCGGCGCGCAGGCG 399

Qy      516 CCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCCGCCGCTGCGCGGAGCCCCACTG 575
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      398 CAGCAGCGCGCGCCACTCGCCCGTCGGGGCGGCCGCTCTCGGGCTCCGTGGCCCGTCC 339

Qy      576 CGAAGCCCAGCTGCGCGCGCCTTGGG 601
          | | | | | | | | | | | | | | | | | |
Db      338 GCCCTCCGGGCAGCCTGCGCCCTCGG 313
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RESULT 6

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US-10-953-349-28773
; Sequence 28773, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28773
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (900)..(900)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-28773
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Query Match          6.2%; Score 39.8; DB 6; Length 1400;
Best Local Similarity 56.5%; Pred. No. 0.44;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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Qy      465 GGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCAGGCCCCACCCCGG 524
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      50  GATGTCGACGGCGACGCGGATGCTGGCGCGCCGCGCCGCCCCGCCCCTCCTCCGCTCCGC 109

Qy      525 GCCCCGCCCCCGAGGCTTAAGCCGCGCCGCGCCCTGCGCGGAGCCCCACTGCGAAGCCCA 584
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```

Db      110 CGCCAGCCCCGGCCTCCTCCGCTCCCCGCCGCCGGCACAGGCCCCAGCCCCGCCCTCGC 169

Qy      585 GCTGCGCGCGC 595
        |||||  ||||
Db      170 GCTGCCGGCGC 180

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RESULT 7

US-11-284-877-17/c

; Sequence 17, Application US/11284877

; Publication No. US20060095984A1

; GENERAL INFORMATION:

; APPLICANT: Hadlaczky, Gyula

; Szalay, Aladar

; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; FOR PREPARING ARTIFICIAL CHROMOSOMES

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 12390 El Camino Real

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92130

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/284,877

; FILING DATE: 21-Nov-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 10/808,689

; FILING DATE: 24-MAR-2004

; APPLICATION NUMBER: 10/219,694

; FILING DATE: 14-AUG-2002

; APPLICATION NUMBER: 10/151,081

; FILING DATE: 16-MAY-2002

; APPLICATION NUMBER: 10/151,078

; FILING DATE: 16-MAY-2002

; APPLICATION NUMBER: 10/125,767

; FILING DATE: 17-APR-2002

; APPLICATION NUMBER: 10/287,313

; FILING DATE: 01-NOV-2002

; APPLICATION NUMBER: 09/799,462

; FILING DATE: 05-MAR-2001

; APPLICATION NUMBER: 09/724,872

; FILING DATE: 28-NOV-2000

; APPLICATION NUMBER: 09/724,726

; FILING DATE: 28-NOV-2000

; APPLICATION NUMBER: 09/724,693

; FILING DATE: 28-NOV-2000

; APPLICATION NUMBER: 08/835,682

; FILING DATE: 10-APR-1997

; APPLICATION NUMBER: 08/695,191

; FILING DATE: 07-AUG-1996

; APPLICATION NUMBER: 08/682,080

; FILING DATE: 15-JUL-1996

; APPLICATION NUMBER: 08/629,822

```

;          FILING DATE: 10-APR-1996
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Seidman, Stephanie L
;          REGISTRATION NUMBER: 33,779
;          REFERENCE/DOCKET NUMBER: 17084-004018/402Q
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 858-678-4777
;          TELEFAX: 202-626-7796
;          TELEX:
;  INFORMATION FOR SEQ ID NO: 17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 42999 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: Genomic DNA
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-284-877-17

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Query Match 6.1%; Score 38.8; DB 7; Length 42999;
 Best Local Similarity 48.6%; Pred. No. 1.5;
 Matches 106; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Qy      387 CGCACGGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCG 446
          | |||| | ||| | || | | || | || | || | || | || |
Db      6431 CCCACGCGGGGGCGAGCGCGGACACCACCCACAGGCGCCCGGGGGTTCCCGCCCCACG 6372

Qy      447 GAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGGCCCCGCC 506
          | || | | || | | || | | || | | || | || | || |
Db      6371 GCGCGGGGCGCACGCCACACGCGCGGCGAGGCGCGCGACGGCCCGCGGGTAAAGCCCCCAC 6312

Qy      507 CCGCAGGCCCCACCCCGGGCCCCGCCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGA 566
          ||| |||| | | ||| || | || ||| |||| | || | |||||
Db      6311 CCGACGGCCGCGCGGGCGGCGGCGGCGGCGGCGGCCCCGCGGGGAGCGGAGTCCGCGGT 6252

Qy      567 GCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATT 604
          | | | | | | | | | | ||| |
Db      6251 GGAGGCGCGGGAGGGGCGGGCCCCCTCCCGACGGGACT 6214

```

RESULT 8

US-10-505-928-53

```

; Sequence 53, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 53
; LENGTH: 1339
; TYPE: DNA

```

; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Human Sox-18
 US-10-505-928-53

Query Match 6.0%; Score 38; DB 6; Length 1339;
 Best Local Similarity 53.3%; Pred. No. 1.1;
 Matches 80; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

Qy      486 GCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAG 545
          ||| | | || ||||| ||| | | | || | ||| | |
Db      233 GCTGACACGCGCGGCTCGCCGCCGGCCCCGCGCCCTCGCCGCGCCCGCCGCGCCCGCC 292

Qy      546 CCGCGCCCGCCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGGGATTG 605
          ||| | | ||| || | || | ||| |||| | || | || | |
Db      293 TCGCCGCCAGCCCGCAGCGCAGTCCCCGCGCAGCCCCGAGCCGGGGCGCTATGGCCTC 352

Qy      606 ACTGTCCACGCTCGCCCGGCTCGTCCGACG 635
          | || || | || | || | ||
Db      353 AGCCCGGCCGGCCGCGGGGAACGCCAGGCG 382
  
```

RESULT 9

US-11-293-697-1028

; Sequence 1028, Application US/11293697
 ; Publication No. US20060105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293,697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIOR APPLICATION NUMBER: US/10/108,260
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1028
 ; LENGTH: 2715
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-293-697-1028

Query Match 6.0%; Score 38; DB 7; Length 2715;
 Best Local Similarity 53.3%; Pred. No. 1.3;
 Matches 80; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

Qy      487 CTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGC 546
          | | | | |||| | || | || | || | | | | | |
Db      1676 CCGGGCGCCCCGGAGCCGAAGCCCGAGCCGAGGAGGTGGCGCTCGCAGCCGCTCTCAGC 1735

Qy      547 CGCGCCGCCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGGGATTGA 606
          | || ||||| |||| | || | || | || | || | || |
Db      1736 CCCGTCGCCCGCGCGCCAAGACCCAGGGAGAGGCGGCGCAGCCGGGCGCTCGGGCTCC 1795

Qy      607 CTGTCCACGCTCGCCCGGCTCGTCCGACGC 636
          | || || || | || | || | ||
Db      1796 GCGCTGCCGGCGCCCCGCCACCCCGCCGC 1825
  
```

RESULT 10

US-10-953-349-30799/c


```
; Sequence 30799, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30799
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-30799
```

```
Query Match          5.9%; Score 37.8; DB 6; Length 461;
Best Local Similarity 51.5%; Pred. No. 1;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
```

```
Qy      451 GCGGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGCCCCGCCCCGC 510
          ||||| || || || || || || || || || || || || || || || || || ||
Db      192 GCGGGCGGCGCGCGACTCGTCTCGCTGGAGGAGGAGTCGGTGGCGTCGGCGTCGTGCACG 133

Qy      511 AGGCCCCACCCCGGGCCCCGCCGCCGAGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCC 570
          || || || || || || || || || || || || || || || || || || || ||
Db      132 ATGATCCGCACCACGCGGCCCTGGGCTGCGCCTCCGCCGAGCCGCCGCCGCCGCCGCC 73

Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCG 619
          || || || || || || || || || || || || || || || || || || || ||
Db      72 TCGGCCGCCGACTCCATCCCCGCGGCGGCGGCCAGCATGTCCAGGCTAG 24
```

RESULT 11

US-10-953-349-31527

```
; Sequence 31527, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31527
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-31527
```

```
Query Match          5.9%; Score 37.6; DB 6; Length 706;
Best Local Similarity 45.8%; Pred. No. 1.2;
Matches 130; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
```

```
Qy      288 CTCACAGAGGTTGGCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTG 347
          ||| || || || || || || || || || || || || || || || || || || ||
Db      121 CTCCGAGCCGTGTGAGAGACGATGAAGAAGGGGGGTCTGCTGCGGTGCGTGTGACGGGG 180
```

```

Qy      348 ACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAG 407
      |  |  || |      || |      ||| |||| |  ||  ||||  || |
Db      181 GCGTGCAGGGTGGCGCCGGGGGCCGTGGCGGAGATGGCCATCTCGCCGACGGCGTCGGGG 240

Qy      408 AAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGT 467
      || ||  || | |  | |  | | || |  |||| |  |  |  || |
Db      241 AAGGTGCCGGCGGGGCACGTGCCGCTGGAGGTGGGCGCGGAGGGGGAGGAGACGGAGCGC 300

Qy      468 CTCCGCACCCAAGTAGGAGCTGGCAGGCCCGCCCCGCCCCGCAGGCCCCACCCCGGGCC 527
      ||| |  | |  | |      | |  ||| |  || |  |  |||||
Db      301 TTCTCGTGCCGGCCGAGCTGCTGGGCCGCCCTCCCATCGCCGAGCTGCTCCGCCGGGCC 360

Qy      528 CCGCCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCC 571
      |||  |      |  |||| || || |  |  |||
Db      361 GCGCAGGAGTACGGCTACGCGCGACGCGGCCCGCTCCGCATCCC 404

```

RESULT 12

US-10-953-349-30799

; Sequence 30799, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 30799

; LENGTH: 461

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-10-953-349-30799

```

Query Match          5.9%; Score 37.4; DB 6; Length 461;
Best Local Similarity 53.0%; Pred. No. 1.2;
Matches 80; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

```

```

Qy      451 GCGGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGCCCCGCCCCGC 510
      ||||| ||| | | | | | | | | | | | | | | | | | |
Db      85 GCGGGCTGCGGCGGAGGCGCAGCCAGGGGCCGCTGGTGCGGATCATCGTGACGACGC 144

Qy      511 AGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCC 570
      | | |||| | | | | |||| | | ||||| ||| | | |
Db      145 CGACGCCACCGACTCCTCCTCAGCGAGGACGAGTCGGCGCCGCGCCGCGCTGGCCAC 204

Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGG 601
      |  ||| | |||  | ||||  ||
Db      205 GATGCCGACGACCAAGGAGGAGCGCCGAGG 235

```

RESULT 13

US-10-953-349-37736

; Sequence 37736, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

```
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37736
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37736
```

```
Query Match          5.9%; Score 37.4; DB 6; Length 1073;
Best Local Similarity 48.7%; Pred. No. 1.5;
Matches 131; Conservative 0; Mismatches 136; Indels 2; Gaps 1;
```

```
Qy      327 GCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGA 386
          ||||| | |||      |||      | |||      || ||  ||  ||
Db      469 GCGGGAGGCGGCGGCTCCCTGAGGCAGTGGTGGCGGGCGGCGTCGTCGGCTGGCTCCTG 528

Qy      387 CGCACGGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCG 446
          | | | |||| | | | | | | | | | | | | | | | | |
Db      529 TCCCGGAAGCCGGGGTTCGCGGGCGACCTCGAGATGAACGAGGACGAGGCCCGCCACGGC 588

Qy      447 GAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGC--CCGGCCCCG 504
          | - ||| ||| | ||| | || | | | | | | | | | | |
Db      589 CAGGGGCACCTGGGGCTGGGGCCACGTCTCTACAGGGTGCCTCCGGCGTCCGCCGCCT 648

Qy      505 CCCCGCAGGCCCCACCCCGGGCCCCGCCGCCGAGGCTTAAGCCGCGCCGCCGCTGCGCG 564
          | || | | | | | | | | | | | | | | | | | | |
Db      649 CGTCGTGTCCGCGCACTCGCTGCCACACGCAGAGGCAGTCCCTGCCGCCGCCGGCGCA 708

Qy      565 GAGCCCCACTGCGAAGCCCAGCTGCGCGC 593
          || | | | | | | | | | |
Db      709 CTGCAAGCCGGCGGCGCTCGCCACGCGC 737
```

RESULT 14

US-11-293-697-208

```
; Sequence 208, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 1354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-208
```

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Query Match          5.9%; Score 37.4; DB 7; Length 1354;
Best Local Similarity 53.0%; Pred. No. 1.5;
Matches 80; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
```

```
Qy      451 GGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGCGC 510
```

```

          | | | | | | | | | | | | | | | | | | | | | |
Db      14  GTCGGCGGCTCCGGGCGCCTCCAGCTCCGGCTCGGGCTCCGGCTCCGGCTCCGGGCGCCG 73

Qy      511 AGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCCCTGCGCGGAGCCC 570
          | | | | | | | | | | | | | | | | | | | | | |
Db      74  ACCAGGTCCCCCTTGGCCCCCGCCGCGCGCCTCCAACCTGCTGCTGCCGCCGCCGCGCCCC 133

Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGG 601
          | | | | | | | | | | | | | | | | | |
Db      134 CCCAGGCTCTGCCAGCTACCCGCGCTCTGAG 164

```

RESULT 15

US-11-312-958-63

; Sequence 63, Application US/11312958

; Publication No. US20060100152A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Rosenfeld, Julie Beth

; APPLICANT: Silos-Santiago, Inmaculada

; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,

; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,

; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,

; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR

; TITLE OF INVENTION: 13424 MOLECULES

; FILE REFERENCE: MPI02-027P1RNOMNIM

; CURRENT APPLICATION NUMBER: US/11/312,958

; CURRENT FILING DATE: 2005-12-20

; PRIOR APPLICATION NUMBER: US/10/369,022

; PRIOR FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: US 60/360,495

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/370,121

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/373,010

; PRIOR FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: US 60/373,908

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 60/377,717

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/379,949

; PRIOR FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/382,409

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 60/385,280

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/386,879

; PRIOR FILING DATE: 2002-06-06

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 63

; LENGTH: 5703

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (213)...(2402)

US-11-312-958-63

Query Match 5.9%; Score 37.4; DB 7; Length 5703;
Best Local Similarity 61.6%; Pred. No. 2.1;
Matches 77; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

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Qy      442 CCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGGCC 501
          ||  |  |  |  |||  ||  |  |  |  |||  |  |  |  |||  |  |||  |||
Db      7  CCCTGCACTAGTGGCCGCAACCGAGACGCCGCGCTCCAGCAGCTGCTGCC--GCCCAGCC 64

Qy      502 CCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCGCCCTGC 561
          |  |||||  ||  |  |||  |  |  |  ||||  ||  |||||  ||  |||  ||
Db      65 CGGCCCCGCGCCGCCCCCAGCCCTGCAGCCCCGCAGCCCCGGCCGCGCCAGCCCGGC 124

Qy      562 GCGGA 566
          |  |||
Db      125 GAGGA 129
```

Search completed: June 6, 2006, 22:25:21
Job time : 26 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09869098 and Search Result us-09-869-098: 1_copy_1634_2270.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 21:25:09 ; Search time 1201 Seconds
(without alignments)
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Title: US-09-869-098A-1_COPY_1634_2270
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	599.8	94.2	9314	7	US-10-197-019-1	Sequence 1, Appli
2	447.4	70.2	1161	7	US-10-265-689-27	Sequence 27, Appl
3	364.2	57.2	5283	7	US-10-311-455-1865	Sequence 1865, Ap
c 4	312.4	49.0	5283	7	US-10-311-455-1866	Sequence 1866, Ap
5	67	10.5	1646	7	US-10-159-563-344	Sequence 344, App
6	67	10.5	1646	10	US-10-287-436A-43	Sequence 43, Appl
7	67	10.5	1646	10	US-10-631-467-426	Sequence 426, App
8	67	10.5	1646	16	US-11-169-041-97	Sequence 97, Appl
9	67	10.5	8177	10	US-10-287-436A-673	Sequence 673, App
c 10	60	9.4	561	12	US-10-301-480-268288	Sequence 268288,
c 11	60	9.4	561	12	US-10-301-480-881697	Sequence 881697,
12	59	9.3	1725	7	US-10-062-674-1405	Sequence 1405, Ap
13	58	9.1	1643	7	US-10-240-965-183	Sequence 183, App
c 14	53	8.3	554	4	US-09-925-065A-177131	Sequence 177131,
c 15	53	8.3	554	5	US-09-925-065A-177131	Sequence 177131,
16	51.8	8.1	2500	7	US-10-190-312A-66	Sequence 66, Appl
17	51.8	8.1	2500	13	US-11-013-031A-66	Sequence 66, Appl
18	51.8	8.1	2500	13	US-11-012-546-66	Sequence 66, Appl
19	50	7.8	946	8	US-10-767-701-9186	Sequence 9186, Ap
20	49	7.7	714	7	US-10-369-493-31991	Sequence 31991, A
c 21	48.4	7.6	4667	9	US-10-723-860-5759	Sequence 5759, Ap
22	48.4	7.6	148083	10	US-10-756-149-4571	Sequence 4571, Ap
23	47.4	7.4	671	6	US-10-184-644-346	Sequence 346, App
24	47.4	7.4	671	6	US-10-184-634-346	Sequence 346, App
25	47.4	7.4	171096	9	US-10-612-869-8	Sequence 8, Appli
c 26	47.2	7.4	863	8	US-10-767-701-6303	Sequence 6303, Ap
c 27	47.2	7.4	1534	8	US-10-437-963-77774	Sequence 77774, A
28	47	7.4	1347	8	US-10-767-701-11203	Sequence 11203, A
c 29	47	7.4	3725	3	US-09-817-910-6	Sequence 6, Appli
c 30	47	7.4	3725	7	US-10-184-648-62	Sequence 62, Appl
c 31	47	7.4	3725	9	US-10-772-636-33	Sequence 33, Appl
c 32	47	7.4	3725	16	US-11-288-493-33	Sequence 33, Appl
c 33	46.4	7.3	1447	8	US-10-437-963-9029	Sequence 9029, Ap
c 34	45.8	7.2	408	10	US-10-450-763-15287	Sequence 15287, A
35	45.6	7.2	594	6	US-10-123-155-10	Sequence 10, Appl
36	45.6	7.2	594	7	US-10-146-731-10	Sequence 10, Appl
37	45.6	7.2	594	7	US-10-140-472-10	Sequence 10, Appl
38	45.6	7.2	594	7	US-10-141-761-10	Sequence 10, Appl
39	45.6	7.2	594	7	US-10-142-885-10	Sequence 10, Appl
40	45.6	7.2	594	7	US-10-158-790-10	Sequence 10, Appl
41	45.6	7.2	594	7	US-10-137-871-10	Sequence 10, Appl
42	45.6	7.2	594	7	US-10-140-923-10	Sequence 10, Appl
43	45.6	7.2	594	7	US-10-141-756-10	Sequence 10, Appl
44	45.6	7.2	594	7	US-10-141-759-10	Sequence 10, Appl
45	45.6	7.2	594	7	US-10-140-805-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-197-019-1

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; Sequence 1, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MWH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1283)..(1283)
; OTHER INFORMATION: PS1: polymorphic base cytosine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1714)..(1714)
; OTHER INFORMATION: PS2: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2051)..(2051)
; OTHER INFORMATION: PS3: polymorphic base thymine or cytosine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2124)..(2124)
; OTHER INFORMATION: PS4: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2287)..(2287)
; OTHER INFORMATION: PS5: polymorphic base cytosine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2408)..(2408)
; OTHER INFORMATION: PS6: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4768)..(4768)
; OTHER INFORMATION: PS7: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4785)..(4785)
; OTHER INFORMATION: PS8: polymorphic base guanine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4813)..(4813)
; OTHER INFORMATION: PS9: polymorphic base thymine or cytosine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (4882)..(4882)
; OTHER INFORMATION: PS10: polymorphic base adenine or cytosine
; FEATURE:
```



```

; NAME/KEY: allele
; LOCATION: (4976)..(4976)
; OTHER INFORMATION: PS11: polymorphic base thymine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (5600)..(5600)
; OTHER INFORMATION: PS12: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (5820)..(5820)
; OTHER INFORMATION: PS13: polymorphic base thymine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (6536)..(6536)
; OTHER INFORMATION: PS14: polymorphic base thymine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (6607)..(6607)
; OTHER INFORMATION: PS15: polymorphic base guanine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (6617)..(6617)
; OTHER INFORMATION: PS16: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (6872)..(6872)
; OTHER INFORMATION: PS17: polymorphic base cytosine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (6966)..(6966)
; OTHER INFORMATION: PS18: polymorphic base guanine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7036)..(7036)
; OTHER INFORMATION: PS19: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7086)..(7086)
; OTHER INFORMATION: PS20: polymorphic base adenine or guanine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (8100)..(8100)
; OTHER INFORMATION: PS21: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (8221)..(8221)
; OTHER INFORMATION: PS22: polymorphic base guanine or adenine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (8677)..(8677)
; OTHER INFORMATION: PS23: polymorphic base thymine or adenine
US-10-197-019-1

```

```

Query Match          94.2%;  Score 599.8;  DB 7;  Length 9314;
Best Local Similarity 98.4%;  Pred. No. 5.7e-164;
Matches 627;  Conservative 0;  Mismatches 7;  Indels 3;  Gaps 2;

```

```

Qy      1  ACCTGTTGCTGCAGTTCTGATTGGTTCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 60
          |||
Db      248 ACCTGTTGCTGCAGTTCTGATTGGTTCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 307

```

```

Qy      61 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
      |||
Db      308 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 367

Qy      121 TCGCAGGAGGGTGGGTAGTTTGTCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
      |||
Db      368 TCGCAGGAGGGTGGGTAGTTTGTCCAGCGTA-GGGGGCTGGGCCCATAAAAGAGGAAGTG 426

Qy      181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
      |||
Db      427 CACTTAAGACACGGCCCCAG--TGGACGCTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 484

Qy      241 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 300
      |||
Db      485 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 544

Qy      301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 360
      |||
Db      545 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 604

Qy      361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAAAGTCATGGAGA 420
      |||
Db      605 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAAAGTCATGGAGA 664

Qy      421 GAACCCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
      |||
Db      665 GAACCCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 724

Qy      481 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGC 540
      |||
Db      725 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGC 784

Qy      541 TTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
      |||
Db      785 TTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 844

Qy      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
      |||
Db      845 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 881

```

RESULT 2

US-10-265-689-27

; Sequence 27, Application US/10265689

; Publication No. US20030119775A1

; GENERAL INFORMATION:

; APPLICANT: SURWIT, RICHARD S.

; APPLICANT: COLLINS, SHEILA A.

; APPLICANT: WARDEN, CRAIG H.

; APPLICANT: SELDIN, MICHAEL F.

; APPLICANT: RICQUIER, DANIEL

; APPLICANT: BOUILLAUD, FREDERIC

; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN

; FILE REFERENCE: 1579-376

; CURRENT APPLICATION NUMBER: US/10/265,689

; CURRENT FILING DATE: 2002-10-08

; PRIOR APPLICATION NUMBER: US/09/353,645

; PRIOR FILING DATE: 1999-07-15

; PRIOR APPLICATION NUMBER: PCT/US97/06864

; PRIOR FILING DATE: 1997-04-22

; PRIOR APPLICATION NUMBER: 60/034,960

Query Match 70.2%; Score 447.4; DB 7; Length 1161;
Best Local Similarity 94.9%; Pred. No. 9.9e-120;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

Qy	100	AGGAGCCAGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCACAGCGT--AGGGGGG	157
Db	2	ANGAACCACCGGCGCGTTCGTTTCGACAGGAGGTGGTTAGTTTGCCAGGGGTAAGGGGGG	61
Qy	158	CTGGGCCCCATAAAAGAGGAAGTGC-ACTTAAGACACGGCCCCGCTGGACGCTGTGTAGAA	216
Db	62	CTGGGCCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCCGTTGGACGCTGTGTAGAA	121
Qy	217	ACCGTCCT-GGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTCTTCT-GGCGGT	274
Db	122	ACCTTCCTGGGTTGGGAAGGCAAGAGGTGTGTGACTGGACAAGAATTGTTCTGGGCGGT	181
Qy	275	CAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAG	334
Db	182	CAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAG	241
Qy	335	TGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGG-	393
Db	242	TGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGA	301
Qy	394	AAACGGGAGTGGAGAAAGTCATGGAGAGAAACCTAGGCGGGGCGGTCCCCGCGGAAAGGC	453
Db	302	AAACGGGAGTGGAGAAAGTCATGGAGAGAAACCTAGGCGGGGCGGTCCCCGCGGAAAGGC	361
Qy	454	GGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGG	513
Db	362	GGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGG	421
Qy	514	CCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCCCTGCGCGGAGCCCCAC	573
Db	422	CCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCCCTGCGCGGAGCCCCAC	481
Qy	574	TGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGA	633
Db	482	TGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGA	541
Qy	634	CGCG 637	
Db	542	CGCG 545	

US-10-311-455-1865
; Sequence 1865, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:

[illegible]

```

Db          479 TTTATTTCGGGTTTCGTTTTTCGAGGTTTAAGTCGCGTCGTCGTTGCGCGGAGTTTTATT 538
Qy          575 GCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGAC 634
          |||||  || ||||| ||||| ||| ||| ||| ||| ||| |||
Db          539 GCGAAGTTTAGTTGCGCGCGTTTTGGGATTGATTGTTTACGTTTCGTTTCGGTTCGTTTCGAC 598
Qy          635 GCG 637
          |||
Db          599 GCG 601

```

RESULT 4

US-10-311-455-1866/c

; Sequence 1866, Application US/10311455

; Publication No. US20030143606A1

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

; APPLICANT: PIEPENBROCK, Christian

; APPLICANT: BERLIN, Kurt

; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete

; TITLE OF INVENTION: cytosine methylation

; FILE REFERENCE: 5013.1014

; CURRENT APPLICATION NUMBER: US/10/311,455

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: PCT/EP01/07537

; PRIOR FILING DATE: 2001-07-02

; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: DE 10043826.1

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 2424

; SEQ ID NO 1866

; LENGTH: 5283

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-1866

```

Query Match          49.0%; Score 312.4; DB 7; Length 5283;
Best Local Similarity 72.0%; Pred. No. 1.8e-80;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

```

```

Qy          34 CCGACAACGCGGCGGCTGTAACCAATCGACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCG 93
          ||||| || || ||||| ||||| ||| ||| ||| ||| ||| |||
Db          5283 CCGACAACGCGACGACTATAACCAATCGACAACGAAACCGATCGCGAAACCCCAATCCCG 5224
Qy          94 CCCTGCAGGAGCCAGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGG 153
          |||| || | ||| ||||| ||||| ||| | || ||| ||| |||
Db          5223 CCCTACAAAAACCAACCGCGCGCTCGCTCGCAAAAAATAAATAATTTACCCAACGTA-A 5165
Qy          154 GGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGTTA 213
          || ||||| || | || | ||||| |||| ||| | |||
Db          5164 AAAACTAAACCCATAAAAAAAAAAATACACTTAAACACGACCC--AATAACGCTATTA 5107
Qy          214 GAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGG 273
          ||||| || || ||| | | ||| ||| ||| ||| ||| |||
Db          5106 AAAACCGTCCTAACTAAAAAACAATAATATATAACTAAACAAACTTATTTCTAACGA 5047
Qy          274 TCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGA 333
          ||| |||| ||||| |||| | || | |||| | | | | | || | ||

```

```

Db      5046 TCAATCTTACCATCTCACAAAAATTAACGACCCGAAAAAATATAAAACAAAAACGAAAA 4987
Qy      334 GTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGG 393
      |   |||   | | ||||| |||   ||||| | ||||| | ||   |||||
Db      4986 ATAACAAAAAATAACCATCTCGAAAAACGAAAAAATAAACGCGATAATAAACGCACGA 4927
Qy      394 AAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGC 453
      ||||| | | | ||| ||| | | ||||| ||   || ||||| ||| |
Db      4926 AAACGAAAATAAAAAAATCATAAAAAAACCTAAACGAAACGATCCCCGCGAAAAAAC 4867
Qy      454 GGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGAGG 513
      | || ||||| ||||| ||||| || | || || |||| ||||| |||||
Db      4866 GACTACTCCAAATCTCCGCACCCAATAAAACTAACAAACCCGACCCCGCCCCGCAA 4807
Qy      514 CCCACCCCCGGGCCCGCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCCAC 573
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4806 CCCACCCCCGAACCCCGCCCCGAACTTAAACCGCGCCGCGCCTACGCGAAACCCAC 4747
Qy      574 TCGGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGA 633
      | |||| |||| || ||||| ||| || ||||| ||||| ||||| |||||
Db      4746 TACGAAACCCAACCTACGCGCGCCTTAAATTAACATCCACGCTCGCCCGACTCGTCCGA 4687
Qy      634 CGCG 637
      ||||
Db      4686 CGCG 4683

```

RESULT 5

US-10-159-563-344

; Sequence 344, Application US/10159563

; Publication No. US20040009154A1

; GENERAL INFORMATION:

; APPLICANT: Khan, Javed

; APPLICANT: Ringner, Markus

; APPLICANT: Peterson, Carsten

; APPLICANT: Meltzer, Paul

; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

; FILE REFERENCE: 11613.56USI1

; CURRENT APPLICATION NUMBER: US/10/159,563

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: US 10/133,937

; PRIOR FILING DATE: 2002-04-25

; NUMBER OF SEQ ID NOS: 444

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 344

; LENGTH: 1646

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-159-563-344

Query Match 10.5%; Score 67; DB 7; Length 1646;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

```

```

Qy      631 CGACGCG 637
      |||||

```

Db 61 CGACGCG 67

RESULT 6

US-10-287-436A-43

; Sequence 43, Application US/10287436A
 ; Publication No. US20050202421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
 ; FILE REFERENCE: 10872.514696
 ; CURRENT APPLICATION NUMBER: US/10/287,436A
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: US 60/336,220
 ; PRIOR FILING DATE: 2001-10-31
 ; NUMBER OF SEQ ID NOS: 1446
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 1646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-287-436A-43

Query Match 10.5%; Score 67; DB 10; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
          |||
Db      1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

Qy      631 CGACGCG 637
          |||
Db      61 CGACGCG 67
```

RESULT 7

US-10-631-467-426

; Sequence 426, Application US/10631467
 ; Publication No. US20050208496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genox Research Inc.
 ; TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
 ; TITLE OF INVENTION: disease
 ; FILE REFERENCE: 3462.1005-000
 ; CURRENT APPLICATION NUMBER: US/10/631,467
 ; CURRENT FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: JP 2003-077212
 ; PRIOR FILING DATE: 2003-03-20
 ; PRIOR APPLICATION NUMBER: JP 2002-229312
 ; PRIOR FILING DATE: 2002-08-06
 ; NUMBER OF SEQ ID NOS: 2086
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 426
 ; LENGTH: 1646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-631-467-426

Query Match 10.5%; Score 67; DB 10; Length 1646;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

Qy      631 CGACGCG 637
          |||||||
Db      61 CGACGCG 67
```

RESULT 8

US-11-169-041-97
; Sequence 97, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-169-041-97

Query Match 10.5%; Score 67; DB 16; Length 1646;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

Qy      631 CGACGCG 637
          |||||||
Db      61 CGACGCG 67
```

RESULT 9

US-10-287-436A-673
; Sequence 673, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31


```
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 673
; LENGTH: 8177
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-673
```

```
Query Match          10.5%; Score 67; DB 10; Length 8177;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCCGGCTCGTC 630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCCGGCTCGTC 60

Qy      631 CGACGCG 637
          |||||||
Db      61 CGACGCG 67
```

RESULT 10

US-10-301-480-268288/c

```
; Sequence 268288, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 268288
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-268288
```

```
Query Match          9.4%; Score 60; DB 12; Length 561;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 ACCTGTTGCTGCAGTTCTGATTGGTTTCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 ACCTGTTGCTGCAGTTCTGATTGGTTTCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 1
```

RESULT 11

US-10-301-480-881697/c

```
; Sequence 881697, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
```

```
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 881697
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-881697
```

```
Query Match          9.4%; Score 60; DB 12; Length 561;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 ACCTGTTGCTGCAGTTCTGATTGGTTCCTTCCCCGACAACGCGGGCTGTAACCAATC 60
        |||
Db      60 ACCTGTTGCTGCAGTTCTGATTGGTTCCTTCCCCGACAACGCGGGCTGTAACCAATC 1
```

RESULT 12

US-10-062-674-1405

```
; Sequence 1405, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1405
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 093687.7
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (1725)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1405
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Query Match          9.3%; Score 59; DB 7; Length 1725;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      579 AGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
        |||
Db      1 AGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 59
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RESULT 13

US-10-240-965-183

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; Sequence 183, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 183
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 093687.6
US-10-240-965-183
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Query Match          9.1%; Score 58; DB 7; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      580 GCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      1   GCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 58
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RESULT 14

US-09-925-065A-177131/c

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; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
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SCORE Search Results Details for Application 09869098 and Search Result us-09-869-098a 1_copy_1634_2270.rni.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 09869098 and Search Result us-09-869-098a 1_copy_1634_2270.rni.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 20:46:25 ; Search time 176 Seconds
(without alignments)
6772.138 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	625	98.1	11808	3	US-09-949-016-15281	Sequence 15281, A
2	625	98.1	39754	3	US-09-949-016-14689	Sequence 14689, A
3	485	76.1	736	2	US-08-846-012A-1	Sequence 1, Appli
4	485	76.1	736	2	US-09-100-297-1	Sequence 1, Appli
5	92.4	14.5	2705	3	US-09-949-016-2947	Sequence 2947, Ap
c 6	60	9.4	7218	2	US-08-232-463-14	Sequence 14, Appl
7	57	8.9	161	3	US-09-513-999C-14461	Sequence 14461, A
c 8	51	8.0	1401	4	US-09-605-703B-543	Sequence 543, App
9	48.4	7.6	69834	3	US-09-949-016-11959	Sequence 11959, A
10	48.4	7.6	69834	3	US-09-949-016-12925	Sequence 12925, A
c 11	45.4	7.1	70014	3	US-09-949-016-17110	Sequence 17110, A
12	44.8	7.0	27270	3	US-09-949-016-13822	Sequence 13822, A
13	44.6	7.0	154746	3	US-09-827-688-8	Sequence 8, Appli
c 14	44.6	7.0	154746	3	US-09-827-688-8	Sequence 8, Appli
c 15	44.4	7.0	670689	3	US-09-949-016-12505	Sequence 12505, A
c 16	44.4	7.0	670690	3	US-09-949-016-14207	Sequence 14207, A
c 17	44	6.9	63183	3	US-09-949-016-13047	Sequence 13047, A
c 18	44	6.9	63183	3	US-09-949-016-13048	Sequence 13048, A
c 19	43.8	6.9	43058	4	US-09-880-107-3950	Sequence 3950, Ap
c 20	43.2	6.8	2592	3	US-09-949-016-2162	Sequence 2162, Ap
21	43.2	6.8	29930	3	US-09-949-016-15326	Sequence 15326, A
c 22	43.2	6.8	43690	3	US-09-949-016-13904	Sequence 13904, A
23	43	6.8	9293	3	US-09-949-016-16801	Sequence 16801, A
24	42.8	6.7	2561	3	US-09-616-289-48	Sequence 48, Appl
25	42.8	6.7	2561	3	US-09-976-740-48	Sequence 48, Appl
c 26	41.8	6.6	4563	3	US-10-012-231A-259	Sequence 259, App
c 27	41.8	6.6	4563	3	US-10-015-389A-259	Sequence 259, App
c 28	41.8	6.6	4563	3	US-10-006-768A-259	Sequence 259, App
c 29	41.8	6.6	4563	3	US-10-015-671A-259	Sequence 259, App
c 30	41.8	6.6	4563	3	US-10-015-393A-259	Sequence 259, App
c 31	41.8	6.6	4563	3	US-10-011-833A-259	Sequence 259, App
c 32	41.8	6.6	4563	3	US-10-006-041A-259	Sequence 259, App
c 33	41.8	6.6	4563	3	US-10-012-064A-259	Sequence 259, App
c 34	41.8	6.6	4563	4	US-10-015-392A-259	Sequence 259, App
c 35	41.8	6.6	4563	5	US-10-011-795B-259	Sequence 259, App
c 36	41.8	6.6	4563	5	US-10-015-386A-259	Sequence 259, App
c 37	41.8	6.6	4563	5	US-10-012-121A-259	Sequence 259, App
c 38	41.8	6.6	4563	5	US-10-006-485A-259	Sequence 259, App
c 39	41.8	6.6	4563	5	US-10-006-746A-259	Sequence 259, App
c 40	41.8	6.6	4563	5	US-10-012-752A-259	Sequence 259, App
c 41	41.8	6.6	4563	5	US-10-017-253A-259	Sequence 259, App
c 42	41.8	6.6	4563	5	US-10-015-519A-259	Sequence 259, App
c 43	41.8	6.6	4563	5	US-10-015-715A-259	Sequence 259, App
c 44	41.8	6.6	4563	5	US-10-007-236A-259	Sequence 259, App
45	41.8	6.6	19152	3	US-09-949-016-12110	Sequence 12110, A

ALIGNMENTS

RESULT 1

US-09-949-016-15281

; Sequence 15281, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15281
; LENGTH: 11808
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15281
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Query Match          98.1%; Score 625; DB 3; Length 11808;
Best Local Similarity 99.8%; Pred. No. 1.8e-131;
Matches 636; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy      1 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGGCTGTAACCAATC 60
      |||
Db    1402 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGGCTGTAACCAATC 1461

Qy      61 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
      |||
Db    1462 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 1521

Qy     121 TCGCAGGAGGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGGCCATAAAAGAGGAAGTG 180
      |||
Db    1522 TCGCAGGAGGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGGCCATAAAAGAGGAAGTG 1581

Qy     181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
      |||
Db    1582 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 1640

Qy     241 GGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 300
      |||
Db    1641 GGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 1700

Qy     301 GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 360
      |||
Db    1701 GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 1760

Qy     361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGA 420
      |||
Db    1761 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGA 1820

Qy     421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
      |||
Db    1821 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGCGGCTGCTCCAGGGTCTCCGCACCCAAG 1880

Qy     481 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGGCCCCGCCCCGAGGC 540
      |||
Db    1881 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGGCCCCGCCCCGAGGC 1940

Qy     541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
      |||
Db    1941 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 2000
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Qy 601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
 |||
 Db 2001 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 2037

RESULT 2

US-09-949-016-14689
 ; Sequence 14689, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 14689
 ; LENGTH: 39754
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(39754)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14689

Query Match 98.1%; Score 625; DB 3; Length 39754;
 Best Local Similarity 99.8%; Pred. No. 2.1e-131;
 Matches 636; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGCGGCTGTAACCAATC 60
 |||
 Db 29317 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGCGGCTGTAACCAATC 29376

Qy 61 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
 |||
 Db 29377 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 29436

Qy 121 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGGCCATAAAAGAGGAAGTG 180
 |||
 Db 29437 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGGCCATAAAAGAGGAAGTG 29496

Qy 181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
 |||
 Db 29497 CACTTAAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 29555

Qy 241 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTGAGTCTTGCCATCCTCACAGAGGTTG 300
 |||
 Db 29556 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTGAGTCTTGCCATCCTCACAGAGGTTG 29615

Qy 301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 360
 |||
 Db 29616 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 29675


```

Qy      361  ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGA 420
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Db      29676 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGA 29735

Qy      421  GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
          |||
Db      29736 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 29795

Qy      481  TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 540
          |||
Db      29796 TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 29855

Qy      541  TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGG 600
          |||
Db      29856 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGG 29915

Qy      601  GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      29916 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 29952

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RESULT 3

US-08-846-012A-1

; Sequence 1, Application US/08846012A

; Patent No. 5807740

; GENERAL INFORMATION:

; APPLICANT: AMARAL, M. Catherine.

; APPLICANT: CHEN, Jin-Long

; TITLE OF INVENTION: Regulators of UCP2 Gene Expression

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,012A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: T97-003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 736 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-846-012A-1

Query Match 76.1%; Score 485; DB 2; Length 736;
 Best Local Similarity 99.6%; Pred. No. 4.1e-100;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy      129 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTAAG 188
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Db      1   GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTAAG 60

Qy      189 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||
Db      61 ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

Qy      249 ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTGGCGGCCCCG 308
          |||
Db      120 ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTGGCGGCCCCG 179

Qy      309 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
          |||
Db      180 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 428
          |||
Db      240 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||
Db      300 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489 GGCAGGCCCCGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCG 548
          |||
Db      359 GGCAGGCCCCGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549 CGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 608
          |||
Db      419 CGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 478

Qy      609 GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479 GTCCACGCTCGCCCGGCTCGTCCGACGCG 507
  
```

RESULT 4

US-09-100-297-1

; Sequence 1, Application US/09100297

; Patent No. 5849514

; GENERAL INFORMATION:

; APPLICANT: AMARAL, M. Catherine.

; APPLICANT: CHEN, Jin-Long

; TITLE OF INVENTION: Regulators of UCP2 Gene Expression

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,297
;      FILING DATE:
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/846,012
;      FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-003
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  736 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
US-09-100-297-1

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Query Match          76.1%;  Score 485;  DB 2;  Length 736;
Best Local Similarity 99.6%;  Pred. No. 4.1e-100;
Matches 507;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

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Qy      129  GGGTGGGTAGTTTGTCCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 188
          |||||||
Db      1    GGGTGGGTAGTTTGTCCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 60

Qy      189  ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||||||
Db      61  ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

Qy      249  ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 308
          |||||||
Db      120  ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 179

Qy      309  AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
          |||||||
Db      180  AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369  GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 428
          |||||||
Db      240  GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429  GGCAGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||||||
Db      300  GGCAGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489  GGCAGGCCCCGCCCCGCCCCGCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 548
          |||||||
Db      359  GGCAGGCCCCGCCCCGCCCCGCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549  CGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 608
          |||||||
Db      419  CGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 478

```

```

Qy      609 GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479 GTCCACGCTCGCCCGGCTCGTCCGACGCG 507

```

RESULT 5

US-09-949-016-2947

; Sequence 2947, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2947

; LENGTH: 2705

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2947

Query Match 14.5%; Score 92.4; DB 3; Length 2705;

Best Local Similarity 98.9%; Pred. No. 1e-11;

Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      544 AGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGAT 603
          | |||
Db      1681 AACCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGAT 1740

```

```

Qy      604 TGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      1741 TGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 1774

```

RESULT 6

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

```

;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/935,313
;   FILING DATE:
;   APPLICATION NUMBER: EP 91 114 300.6
;   FILING DATE: 26-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BENT, Stephen A.
;   REGISTRATION NUMBER: 29,768
;   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703)836-9300
;   TELEFAX: (703)683-4109
;   TELEX: 899149
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 7218 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   CLONE: pTZgpt-Fls
US-08-232-463-14

```

Query Match 9.4%; Score 60; DB 2; Length 7218;
 Best Local Similarity 4.4%; Pred. No. 0.00022;
 Matches 18; Conservative 230; Mismatches 160; Indels 0; Gaps 0;

```

Qy      117 TCGCTCGCAGGAGGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGA 176
        | | |: ::::: : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1440 TGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1381

Qy      177 AGTGCACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGC 236
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1380 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1321

Qy      237 AAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAG 296
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1320 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1261

Qy      297 GTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCG 356
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1260 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1201

Qy      357 GGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATG 416
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1200 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1141

Qy      417 GAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACC 476
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1140 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1081

Qy      477 CAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGAGGCCCCACCCCGG 524

```

```

          ::: :::: : : || | | || | | | | | | | | |
Db      1080 RRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGG 1033

```

RESULT 7

```

US-09-513-999C-14461
; Sequence 14461, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14461
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: s=g or c
US-09-513-999C-14461

```

```

Query Match          8.9%; Score 57; DB 3; Length 161;
Best Local Similarity 96.6%; Pred. No. 0.00068;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      579 AGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          | :|||||
Db      9  AASCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 67

```

RESULT 8

```

US-09-605-703B-543/c
; Sequence 543, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 543

```

```

;   LENGTH: 1401
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1378)
;   OTHER INFORMATION: RXN01229
;   NAME/KEY: VARIANT
;   LOCATION: 119
;   OTHER INFORMATION: Xaa = Tyr or Ser
;   NAME/KEY: VARIANT
;   LOCATION: 120
;   OTHER INFORMATION: Xaa = Asn, Thr, His, or Pro
;   NAME/KEY: VARIANT
;   LOCATION: 121, 266
;   OTHER INFORMATION: Xaa = Glu or Val
;   NAME/KEY: VARIANT
;   LOCATION: 122, 303
;   OTHER INFORMATION: Xaa = Asn or Thr
;   NAME/KEY: VARIANT
;   LOCATION: 123, 301
;   OTHER INFORMATION: Xaa = Glu, Asp, Gln, or Pro
;   NAME/KEY: VARIANT
;   LOCATION: 124, 265
;   OTHER INFORMATION: Xaa = Glu, Ala, Lys, or Asn
;   NAME/KEY: VARIANT
;   LOCATION: 125
;   OTHER INFORMATION: Xaa = Glu, Ala, His, Pro, or Gln
;   NAME/KEY: VARIANT
;   LOCATION: 126, 239, 283
;   OTHER INFORMATION: Xaa = Ala
;   NAME/KEY: VARIANT
;   LOCATION: 127, 251
;   OTHER INFORMATION: Xaa = Glu, Ala, Asp, Lys, Thr, or Asn
;   NAME/KEY: VARIANT
;   LOCATION: 128
;   OTHER INFORMATION: Xaa = Ile or Thr
;   NAME/KEY: VARIANT
;   LOCATION: 129
;   OTHER INFORMATION: Xaa = Gly or Glu
;   NAME/KEY: VARIANT
;   LOCATION: 130
;   OTHER INFORMATION: Xaa = Lys, Ile, or Asn
;   NAME/KEY: VARIANT
;   LOCATION: 132
;   OTHER INFORMATION: Xaa = Lys, Gln, Asn, or His
;   NAME/KEY: VARIANT
;   LOCATION: 175
;   OTHER INFORMATION: Xaa = Leu or Ser
;   NAME/KEY: VARIANT
;   LOCATION: 178, 230, 295
;   OTHER INFORMATION: Xaa = Ile or Leu
;   NAME/KEY: VARIANT
;   LOCATION: 180, 211
;   OTHER INFORMATION: Xaa = Pro
;   NAME/KEY: VARIANT
;   LOCATION: 181, 223, 244
;   OTHER INFORMATION: Xaa = Ala or Ser
;   NAME/KEY: VARIANT
;   LOCATION: 187
;   OTHER INFORMATION: Xaa = Val

```

```

; NAME/KEY: VARIANT
; LOCATION: 188, 198, 219, 302, 306
; OTHER INFORMATION: Xaa = Gly or Val
; NAME/KEY: VARIANT
; LOCATION: 193
; OTHER INFORMATION: Xaa = Val or Leu
; NAME/KEY: VARIANT
; LOCATION: 204, 282
; OTHER INFORMATION: Xaa = Ala or Thr
; NAME/KEY: VARIANT
; LOCATION: 205
; OTHER INFORMATION: Xaa = Gln or Pro
; NAME/KEY: VARIANT
; LOCATION: 206, 220,
; OTHER INFORMATION: Xaa = Val or Ile
; NAME/KEY: VARIANT
; LOCATION: 207
; OTHER INFORMATION: Xaa = Ser or Pro
; NAME/KEY: VARIANT
; LOCATION: 210, 298
; OTHER INFORMATION: Xaa = Phe or Ser
; NAME/KEY: VARIANT
; LOCATION: 214, 238, 243, 252, 257, 269
; OTHER INFORMATION: Xaa = Gly or Ala
; NAME/KEY: VARIANT
; LOCATION: 216, 217, 225, 249, 258, 319
; OTHER INFORMATION: Xaa = Gly or Arg
; NAME/KEY: VARIANT
; LOCATION: 218, 236
; OTHER INFORMATION: Xaa = Leu or Phe
; NAME/KEY: VARIANT
; LOCATION: 221, 286
; OTHER INFORMATION: Xaa = Gly
; NAME/KEY: VARIANT
; LOCATION: 226, 299
; OTHER INFORMATION: Xaa = Leu or Pro
; NAME/KEY: VARIANT
; LOCATION: 234
; OTHER INFORMATION: Xaa = Lys or Thr
; NAME/KEY: VARIANT
; LOCATION: 235
; OTHER INFORMATION: Xaa = Gln or Leu
; NAME/KEY: VARIANT
; LOCATION: 237, 291
; OTHER INFORMATION: Xaa = Gly, Val, Trp, Leu, Cys, or Phe
; NAME/KEY: VARIANT
; LOCATION: 240, 256
; OTHER INFORMATION: Xaa = Val or Ala
; NAME/KEY: VARIANT
; LOCATION: 241, 254
; OTHER INFORMATION: Xaa = Val, Leu, or Phe
; NAME/KEY: VARIANT
; LOCATION: 242
; OTHER INFORMATION: Xaa = Gly, Cys, or STOP codon
; NAME/KEY: VARIANT
; LOCATION: 245
; OTHER INFORMATION: Xaa = Gly, Ala, Trp, Ser, or STOP codon
; NAME/KEY: VARIANT
; LOCATION: 247
; OTHER INFORMATION: Xaa = Lys or Gln
; NAME/KEY: VARIANT

```



```

; LOCATION: 248
; OTHER INFORMATION: Xaa = Arg or Lys
; NAME/KEY: VARIANT
; LOCATION: 250
; OTHER INFORMATION: Xaa = Gly, Glu, Arg, Lys, Asp, Asn,
; OTHER INFORMATION: or Ser
; NAME/KEY: VARIANT
; LOCATION: 253
; OTHER INFORMATION: Xaa = Gly, Val, Cys, or Phe
; NAME/KEY: VARIANT
; LOCATION: 259
; OTHER INFORMATION: Xaa = Cys, Phe, Arg, or Leu
; NAME/KEY: VARIANT
; LOCATION: 260, 310
; OTHER INFORMATION: Xaa = Cys or Phe
; NAME/KEY: VARIANT
; LOCATION: 261, 262
; OTHER INFORMATION: Xaa = Arg
; NAME/KEY: VARIANT
; LOCATION: 263, 296
; OTHER INFORMATION: Xaa = Arg or Leu
; NAME/KEY: VARIANT
; LOCATION: 264, 289
; OTHER INFORMATION: Xaa = Glu, Val, Asp, Gln, Leu,
; OTHER INFORMATION: or His
; NAME/KEY: VARIANT
; LOCATION: 267
; OTHER INFORMATION: Xaa = Val, Met, or Ile
; NAME/KEY: VARIANT
; LOCATION: 268
; OTHER INFORMATION: Xaa = Gly, Val, Ser, or Ile
; NAME/KEY: VARIANT
; LOCATION: 270
; OTHER INFORMATION: Xaa = Asp or Ala
; NAME/KEY: VARIANT
; LOCATION: 271
; OTHER INFORMATION: Xaa = Asp, Val, His, or Leu
; NAME/KEY: VARIANT
; LOCATION: 272
; OTHER INFORMATION: Xaa = Leu
; NAME/KEY: VARIANT
; LOCATION: 273, 307
; OTHER INFORMATION: Xaa = Val, Ala, Leu, or Pro
; NAME/KEY: VARIANT
; LOCATION: 274
; OTHER INFORMATION: Xaa = Asp, Ala, or Glu
; NAME/KEY: VARIANT
; LOCATION: 275
; OTHER INFORMATION: Xaa = Thr or His
; NAME/KEY: VARIANT
; LOCATION: 276
; OTHER INFORMATION: Xaa = Gln, His, or Pro
; NAME/KEY: VARIANT
; LOCATION: 277, 278, 285
; OTHER INFORMATION: Xaa = Gly, Pro, Arg, or Ala
; NAME/KEY: VARIANT
; LOCATION: 279, 284
; OTHER INFORMATION: Xaa = Ala or Pro
; NAME/KEY: VARIANT

```

Query Match 8.0%; Score 51; DB 4; Length 1401;

Best Local Similarity 14.0%; Pred. No. 0.02;
Matches 36; Conservative 123; Mismatches 98; Indels 0; Gaps 0;

```

Qy      318 GAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCG 377
      | ||| : :|: :::: : : | :|::: : : : : : : : :
Db      1061 GTGGCCYWMYYSGKWRKYSKYYTYYYMRRAAMAWYYMWWRSMMCMRKKKKGKTWMCYK 1002

Qy      378 GTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCG 437
      : : :|: : : | :| : : : : : : | :|::: : : : : :| :
Db      1001 SCSGRRGRRAAAMRMGWAKWSWSMSSSRSMYAWMWSKSGMSMSCCKSSKGSRGCRGYSS 942

Qy      438 GTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCC 497
      :|: :::: : : :::|: : : ||: ||: : : | : : : : : : |
Db      941 WYCMWGSMSSCSSMKGRTSKKCWRSRAGGWSGKCGSCGMYSAYYWCKTYSWSSMGKCGWC 882

Qy      498 GGCCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCGAGGCTTAAGCCGCGCCGCCGC 557
      | : :::|::|: | |:: : : : : : :|: : :|::| |::
Db      881 GAMAAMRMCMSMCMRCCACMAMMMSCMKYMYCCYYTYTKTYYYSMSGMRSCWCMKA 822

Qy      558 CTGCGCGGAGCCCCACT 574
      :::|: : :::| |
Db      821 MWRCKGCSSCSMMSAAT 805
    
```

RESULT 9

```

US-09-949-016-11959
; Sequence 11959, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11959
; LENGTH: 69834
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69834)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11959
    
```

Query Match 7.6%; Score 48.4; DB 3; Length 69834;
Best Local Similarity 52.5%; Pred. No. 0.12;
Matches 106; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

```

Qy      436 CGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGC 495
      || |||| | || | | | || |||| | || | |||
Db      38656 CGTCCCCTGCCACCCCCGCCCTGCGACCCTGCCCAGCCCAGCCTAGCGCAGCCCGGC 38715
    
```

```

Qy      496 CCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCC 555
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38716 CAGGCCCCGCGCGGGGGGCGCCGTCCCGCCCCGCCCGAGCCCGTACCCGCCGCGGC 38775

Qy      556 GCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACG 615
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38776 GCCGGTGCCTACGCTGCGTCAGGGCCGCGCCCCGCGCGACGTCGCTGCCTCGCGGCCCC 38835

Qy      616 CTCGCCCCGGCTCGTCCGACGCG 637
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38836 GCCCCCAGGCCCGACATCCTCG 38857

```

RESULT 10

US-09-949-016-12925

; Sequence 12925, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12925

; LENGTH: 69834

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(69834)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12925

```

Query Match          7.6%;  Score 48.4;  DB 3;  Length 69834;
Best Local Similarity 52.5%;  Pred. No. 0.12;
Matches 106;  Conservative 0;  Mismatches 96;  Indels 0;  Gaps 0;

```

```

Qy      436 CGGTCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGC 495
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38656 CGTCCCCTGCCACCCCCGCCCCCTGCGACCCTGCCCGAGCCAGCCTAGCGCAGCCCGGC 38715

Qy      496 CCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCC 555
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38716 CAGGCCCCGCGCGGGGGGCGCCGTCCCGCCCCGCCCGAGCCCGTACCCGCCGCGGC 38775

Qy      556 GCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACG 615
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38776 GCCGGTGCCTACGCTGCGTCAGGGCCGCGCCCCGCGCGACGTCGCTGCCTCGCGGCCCC 38835

Qy      616 CTCGCCCCGGCTCGTCCGACGCG 637
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38836 GCCCCCAGGCCCGACATCCTCG 38857

```

RESULT 11

US-09-949-016-17110/c

; Sequence 17110, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17110

; LENGTH: 70014

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(70014)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17110

Query Match 7.1%; Score 45.4; DB 3; Length 70014;

Best Local Similarity 47.6%; Pred. No. 0.57;

Matches 165; Conservative 0; Mismatches 181; Indels 1; Gaps 1;

```

Qy      248 GACTGGACAAGACTTGTCTTCTGGCGGTCTGCTTCCATCCTCACAGAGGTTGGCGGCC 307
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2224 GCCTGCAGCGAGCGCGGCTCCGGCGGAGGTCCCGGGCAGGCTCCGGGCGCCAGGCGCGAG 2165

Qy      308 GAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGG 367
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2164 CAGAGAAGGCGGAGACGCGGCCTCCGGTTGCCAGGTGCGCGTCTCCACGCAGAGGCCAG 2105

Qy      368 AGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCT 427
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2104 GTAGGAGGAGGAGAAGGGGCGGGGAGAAAAGGAGGACGCTTGACCCGCTTTAGCGCGGCT 2045

Qy      428 AGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGC 487
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2044 CTGGGCTCCCGCCGCCCGCGCAGGCCCTCCCGCCCCGCCCCCGGAGCCGGACTCGGAGC 1985

Qy      488 TGGCAGGCCCCGGCCCCGCCCCGCGAGCCCCACCCCGGGCCCCGCCCCCGAGG-CTTAAGC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1984 CGGCTTGTCGGCCCCGCGACACTTCTCCCTGCCGGGCTCCCGCACCAAGGTCTCGCGC 1925

Qy      547 CGCGCCCGCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGC 593
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1924 CGCAGGCCCCGCCCCCTGCGCTGCACTGCGGTTCCACAGCCCCGC 1878

```

RESULT 12

US-09-949-016-13822
; Sequence 13822, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13822
; LENGTH: 27270
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13822

Query Match 7.0%; Score 44.8; DB 3; Length 27270;
Best Local Similarity 45.1%; Pred. No. 0.69;
Matches 210; Conservative 0; Mismatches 252; Indels 4; Gaps 1;

Qy	40	ACGCGGCGGCTGTAAACCAATCGACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGC	99
Db	1130	ACATGGGGGGTGTGAGGTGGGGACAGGCAGGGAGATGGGGGGTGCGAGGTGGGGACAAGC	1189
Qy	100	AGGAGCCAGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGTCCAGCGTAGGGGGGCT	159
Db	1190	AGGGACATGGGGAGTGCAGGTGGGGACAGGCAGGGACGTGGGGCGTGCGAGGTGGGGAC	1249
Qy	160	GGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACC	219
Db	1250	AGGCAGGGACATAAGGGTGTGAGGTGGAGACAGGCAGGGACATGGGGAGTCTGAGGTGGG	1309
Qy	220	GTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTC	279
Db	1310	GACAGGCAGGGAGATGGGGGGTGTGAGTTGGGGACAGGCAGGGAGATGGGGGGGTGCGAG	1369
Qy	280	TTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCA	339
Db	1370	GTGGGGATAAGCAGGGACATGGGGGTGCGAGGTGGGGACAGGCAGGGACATGGGGGTGGG	1429
Qy	340	AGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGG----TGATGGGACGCACGGAA	395
Db	1430	AGGTGGGGACAGGCAGGGACATAGGGGGTGGGAGGTGGGCACATTCAGGGAGATGGGGGT	1489
Qy	396	ACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGG	455
Db	1490	GTGAGGTGGGAGACAGGCAGGGACATAGGGGGAGCGAGGTGGGGACAGGCAGGGAGATGG	1549
Qy	456	CTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCC	501
Db	1550	AGGGTGCAAGGTGAAGACAGGCAGGGACATGGTGTGAGGTGGGGAC	1595

RESULT 13

US-09-827-688-8

; Sequence 8, Application US/09827688

; Patent No. 6821955

; GENERAL INFORMATION:

; APPLICANT: ORSON, FRANK

; APPLICANT: KINSEY, BERMA

; APPLICANT: BHOGAL, BALBIR

; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION

; TITLE OF INVENTION: AGENTS

; FILE REFERENCE: P01949US1/10004014

; CURRENT APPLICATION NUMBER: US/09/827,688

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/195,680

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 154746

; TYPE: DNA

; ORGANISM: HERPESVIRUS 2

US-09-827-688-8

Query Match 7.0%; Score 44.6; DB 3; Length 154746;

Best Local Similarity 50.2%; Pred. No. 0.94;

Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Qy      418 AGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCC 477
          |||  ||  |  |  |||  |  |  |  ||  ||  ||  ||  |  |  |||
Db      127637 AGAGCCCCAGACCCCCCGCGGGCGCGGGAGACGTGCCGCCGCCCGACCCCCGCCCCGCC 127696

Qy      478 AAGTAGGAGCTGGCAGGCCCCGCCCCGCCCCGAGCCCCACCCCGGGCCCCGCCCCCGA 537
          |  |  |  |  |  |||  |||  ||  |  |  |||  |||  |||  |
Db      127697 GACCCCCGCCCCGCCCCGACCCCCGCCCCGCCCCGACCCCCGCCCCGACCCCCGCCCCGCC 127756

Qy      538 GGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCT 597
          |  |  |||  |||  |  |  |  |  |  |  |  |  |  |  |||  |||
Db      127757 GACCCCCGCCCCGCCCCGACCCCCGCCCCGCCCCGACCCCCGCCCCGACCCCCGCCCCGCC 127816

Qy      598 TGGGATTGACTGTCCACGCTCGCCCCGGCTCGTCCGACGC 636
          |  |  ||  |  |  ||  ||  ||  ||  ||  ||
Db      127817 GACCCCCGCCCCGCCCCGACCCCCGCCCCGCCCCGACCCCCGC 127855

```

RESULT 14

US-09-827-688-8/c

; Sequence 8, Application US/09827688

; Patent No. 6821955

; GENERAL INFORMATION:

; APPLICANT: ORSON, FRANK

; APPLICANT: KINSEY, BERMA

; APPLICANT: BHOGAL, BALBIR

; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION

; TITLE OF INVENTION: AGENTS

; FILE REFERENCE: P01949US1/10004014

; CURRENT APPLICATION NUMBER: US/09/827,688

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/195,680

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8
 ; LENGTH: 154746
 ; TYPE: DNA
 ; ORGANISM: HERPESVIRUS 2
 US-09-827-688-8

Query Match 7.0%; Score 44.6; DB 3; Length 154746;
 Best Local Similarity 50.2%; Pred. No. 0.94;
 Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

```

Qy      418 AGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCC 477
          |||| || | | |||| | | | | || || || || || || || || || || ||
Db      154105 AGAGCCCAGACCCCCCGCGGGCGCGGGAGACGTGCCGCCCGCCCGACCCCCGCCCGCCC 154046

Qy      478 AAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGAGGCCCCACCCCGGGCCCCCGCCCCGA 537
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      154045 GACCCCCGCCCGCCCCGACCCCCGCCCGCCCGACCCCCGCCCGCCCGACCCCCGCCCGCCC 153986

Qy      538 GGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCT 597
          | | ||| ||| | | | | | | | | | | | | | | | | | | | | |
Db      153985 GACCCCCGCCCGCCCCGACCCCCGCCCGCCCGACCCCCGCCCGCCCGACCCCCGCCCGCCC 153926

Qy      598 TGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGC 636
          | | | | | | | | | | | | | | | | | | | | |
Db      153925 GACCCCCGCCCGCCCCGACCCCCGCCCGCCCGACCCCCGC 153887

```

RESULT 15

US-09-949-016-12505/c
 ; Sequence 12505, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12505
 ; LENGTH: 670689
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(670689)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-12505

Query Match 7.0%; Score 44.4; DB 3; Length 670689;
 Best Local Similarity 54.2%; Pred. No. 1.2;
 Matches 90; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

```

Qy      431 CGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGG 490

```

```

      || | || |||| ||| | || ||| | || | | |
Db      40337 CGCGCCGCCCCCCCCCGGCCCCCGCGACGCCCCACCCACCCCGCCCCCGCCCGCACCCC 40278
Qy      491 CAGGCCCCGCCCCGCCCCGCAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCGCG 550
      | |||| | || | | | |||| || | || ||| | || | |||||
Db      40277 CCGGCCAGCACCCCCGACCCGCGCCCCCGCCCCCGCCCCCGCCCGCACGCCACGCCGCG 40218
Qy      551 CCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCC 596
      || ||||| | | |||| | | || | || ||||
Db      40217 CCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGCCGGGCC 40172
```

Search completed: June 6, 2006, 20:53:54
Job time : 179 secs

SCORE 1.3 BuildDate: 12/06/2005

Comments /
Suggestions

start

[Go Back to previous page](#)

OM nucleic - nucleic search, using sw model

Title: US-09-869-098A-1_COPY_1634_2270
Perfect score: 637
Sequence: 1 acctgtttgctgcagtcttga.....cgccccggctcgctccgacgcg 637

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : N_Geneseq_8:*
1:  geneseqn1980s:*
2:  geneseqn1990s:*
3:  geneseqn2000s:*
4:  geneseqn2001as:*
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6:  geneseqn2002as:*
7:  geneseqn2002bs:*
8:  geneseqn2003as:*
9:  geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	637	100.0	3505	3	AAA62932	Aaa62932 DNA conta
2	599.8	94.2	9314	12	ADG65405	Adg65405 Human unc
3	485	76.1	736	2	AAV44974	Aav44974 UCP2 gene
4	485	76.1	736	2	AAV08879	Aav08879 UCP2 prom
5	447.4	70.2	1161	2	AAV44599	Aav44599 Human unc
6	364.2	57.2	5283	6	ABL33892	Abl33892 Human imm
c 7	312.4	49.0	5283	6	ABL33893	Abl33893 Human imm
8	67	10.5	1646	11	ADP64964	Adp64964 Human unc
9	67	10.5	1646	12	ADJ75174	Adj75174 Marker ge
10	67	10.5	1646	14	ADY16091	Ady16091 DNA encod
11	67	10.5	8177	11	ADP65417	Adp65417 Human unc
12	58	9.1	1643	6	AAS94928	Aas94928 Human DNA
13	57	8.9	161	3	AAC10386	Aac10386 Human sec
14	51.8	8.1	2500	10	ADB87421	Adb87421 Transgene
15	51.8	8.1	2500	12	ADJ35230	Adj35230 Human sta
16	51.8	8.1	2500	12	ADL96848	Adl96848 STablizin
c 17	51	8.0	1401	14	AED70367	Aed70367 Corynebac
18	50.8	8.0	10732	3	AAA10594	Aaa10594 Gene enco
19	49	7.7	714	13	ADS56317	Ads56317 Bacterial
c 20	48.4	7.6	4667	12	ADQ22939	Adq22939 Human sof
c 21	47.4	7.4	2365	6	ABZ33727	Abz33727 Human TRI
22	47.4	7.4	171096	13	ADT05874	Adt05874 Cercopith
c 23	47	7.4	3725	4	AAH27094	Aah27094 Human acy
c 24	47	7.4	3725	13	ADR40152	Adr40152 Human lys
25	46.6	7.3	2986	8	ABZ80413	Abz80413 Human pro
26	46.4	7.3	39949	12	ADF31997	Adf31997 Full leng
27	46.4	7.3	48200	12	ADF31998	Adf31998 Cosmid 2A
c 28	46.2	7.3	2890	13	ADR07917	Adr07917 Full leng
c 29	45.8	7.2	408	5	AAS79483	Aas79483 DNA encod
c 30	45.8	7.2	2452	13	ACN42716	Acn42716 Human dia
c 31	45.8	7.2	2506	13	ACN42715	Acn42715 Human dia
c 32	45.8	7.2	2512	13	ACN42714	Acn42714 Human dia
c 33	45	7.1	4565	10	ABX95723	Abx95723 DNA encod
c 34	45	7.1	4565	12	ADI37007	Adi37007 Novel hum
c 35	45	7.1	4565	12	ADL82988	Adl82988 Human PRO
c 36	45	7.1	4565	12	ADL91794	Adl91794 Human PRO
c 37	45	7.1	4565	13	ADP56159	Adp56159 Human PRO
c 38	45	7.1	4565	14	ADY14975	Ady14975 DNA encod
c 39	45	7.1	4565	14	ADY20007	Ady20007 DNA encod
c 40	45	7.1	4566	3	AAC74710	Aac74710 Human ORF
c 41	45	7.1	4607	5	ABV28262	Abv28262 Human pro
c 42	45	7.1	5171	12	ADQ23208	Adq23208 Human sof
c 43	44.8	7.0	2413	13	ADT20125	Adt20125 Plant cDN
44	44.6	7.0	1281	2	AAQ23296	Aaq23296 HSV-1 (MG
c 45	44.6	7.0	114955	2	AAX53491	Aax53491 Human ade

ALIGNMENTS

RESULT 1
AAA62932

ID AAA62932 standard; DNA; 3505 BP.
 XX
 AC AAA62932;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE DNA containing human uncoupling protein-2 (UCP-2) promoter region.
 XX
 KW Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
 KW hypotension; hyperlipidaemia; anti-pyretic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200039315-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-JP007198.
 XX
 PR 24-DEC-1998; 98JP-00366719.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Toyoda Y, Kobayashi M, Igaki S;
 XX
 DR WPI; 2000-452407/39.
 XX
 PT DNA with promoter region containing regulator sequence of uncoupling
 PT protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,
 PT hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in
 PT therapy.
 XX
 PS Claim 4; Fig 1-6; 43pp; Japanese.
 XX
 CC This invention relates to DNA comprising a promoter region containing the
 CC regulatory sequences of human uncoupling protein-2 (UCP-2). Included in
 CC the invention are a recombinant vector containing the DNA sequence, cells
 CC transformed by the vector, and a method for screening for compounds or
 CC salts that can promote or inhibit the UCP-2 promoter activity using the
 CC transformants. The DNA and cells transformed using it can be used to
 CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidaemic
 CC and anti-pyretic drugs. The present sequence represents DNA containing
 CC the UCP-2 promoter sequences
 XX
 SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 637; DB 3; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 3.4e-133;
 Matches 637; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACCTGTTGCTGCAGTTCTGATTGGTTCTCTCCCCGACAACGCGGCGGCTGTAACCAATC	60
Db	1634	ACCTGTTGCTGCAGTTCTGATTGGTTCTCTCCCCGACAACGCGGCGGCTGTAACCAATC	1693
Qy	61	GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC	120
Db	1694	GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC	1753
Qy	121	TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG	180
Db	1754	TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG	1813

```

Qy      181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
          |||
Db      1814 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 1873

Qy      241 GGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 300
          |||
Db      1874 GGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 1933

Qy      301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 360
          |||
Db      1934 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 1993

Qy      361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 420
          |||
Db      1994 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 2053

Qy      421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
          |||
Db      2054 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 2113

Qy      481 TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 540
          |||
Db      2114 TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 2173

Qy      541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
          |||
Db      2174 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 2233

Qy      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      2234 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 2270

```

RESULT 2

ADG65405

ID ADG65405 standard; DNA; 9314 BP.

XX

AC ADG65405;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human uncoupling protein 2 (UCP2) gene.

XX

KW anorectic; antidiabetic; immunomodulator; gene therapy; haplotyping;

KW uncoupling protein 2; mitochondrial; proton carrier; UCP2;

KW polymorphic site; haplotype; haplotype pair; obesity; diabetes;

KW immunological disorder; body mass defect; thermoregulation defect; human;

KW gene; ds; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation 1283

FT /*tag= a

FT /standard_name= "Single nucleotide polymorphism"

FT variation 1714

FT /*tag= b

FT /standard_name= "Single nucleotide polymorphism"

FT variation 2051

FT /*tag= c

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FT		/*tag= d
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FT	variation	2408
FT		/*tag= f
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	4768
FT		/*tag= g
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	4785
FT		/*tag= h
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	4813
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FT	variation	4882
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FT	variation	4976
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FT		/*tag= m
FT		/product= "Uncoupling protein 2"
FT	exon	5281. .5406
FT		/*tag= l
FT		/number= 1
FT	intron	5407. .5562
FT		/*tag= n
FT		/number= 1
FT	exon	5563. .5773
FT		/*tag= o
FT		/number= 2
FT	variation	5600
FT		/*tag= p
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FT	intron	5774. .6641
FT		/*tag= q
FT		/number= 2
FT	variation	5820
FT		/*tag= r
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FT	variation	6536
FT		/*tag= s
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	6607
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FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	6617
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FT		/standard_name= "Single nucleotide polymorphism"
FT	exon	6642. .6836
FT		/*tag= v
FT		/number= 3
FT	intron	6837. .6916
FT		/*tag= w
FT		/number= 3

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FT      variation      6872
FT      /*tag= x
FT      /standard_name= "Single nucleotide polymorphism"
FT      exon           6917. .7018
FT      /*tag= y
FT      /number= 4
FT      variation      6966
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FT      /standard_name= "Single nucleotide polymorphism"
FT      intron         7019. .7984
FT      /*tag= aa
FT      /number= 4
FT      variation      7036
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FT      variation      7086
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FT      /standard_name= "Single nucleotide polymorphism"
FT      exon           7985. .8165
FT      /*tag= ad
FT      /number= 5
FT      variation      8100
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FT      /number= 6
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XX
PN      US2003207284-A1.
XX
PD      06-NOV-2003.
XX
PF      16-JUL-2002; 2002US-00197019.
XX
PR      25-JAN-2001; 2001WO-US002485.
XX
PA      (CHEW/) CHEW A.
PA      (DENT/) DENTON R R.
PA      (GILS/) GILSON C R.
PA      (NAND/) NANDABALAN K.
PA      (PARK/) PARKS K E.
XX
PI      Chew A, Denton RR, Gilson CR, Nandabalan K, Parks KE;
XX
DR      WPI; 2004-051505/05.
DR      P-PSDB; ADG65407.
XX
PT      Haplotyping Uncoupling Protein 2 gene of an individual comprises
PT      identifying the phased sequence of nucleotides at polymorphic sites of
PT      the gene and assigning a haplotype or haplotype pair consistent with the
PT      phased sequence.
XX

```



```

Qy      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      845 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 881

```

RESULT 3

AAV44974

ID AAV44974 standard; cDNA; 736 BP.

XX

AC AAV44974;

XX

DT 16-NOV-1998 (first entry)

XX

DE UCP2 gene transcriptional promoter sequence.

XX

KW Uncoupling protein 2; UCP2 gene; transcriptional promoter; mouse;

KW mitochondrial protein; cis transcriptional regulatory activity; therapy;

KW expression modulator screening; fat feeding; diabetes; obesity; ds.

XX

OS Mus sp.

XX

PN US5807740-A.

XX

PD 15-SEP-1998.

XX

PF 25-APR-1997; 97US-00846012.

XX

PR 25-APR-1997; 97US-00846012.

XX

PA (TULA-) TULARIK INC.

XX

PI Chen J, Amaral MC;

XX

DR WPI; 1998-520130/44.

XX

PT Mouse UCP2 gene promoter - useful for forming transfected cell lines

PT employed in drug screening assays.

XX

PS Claim 1; Col 7-8; 9pp; English.

XX

CC This sequence represents the mouse mitochondrial uncoupling protein 2
 CC (UCP2) gene transcriptional promoter of the invention. The promoter has
 CC cis transcriptional regulatory activity. Cells containing the promoter
 CC attached to a non-UCP2 gene, in which the non-UCP2 gene is a reporter
 CC gene can be used in screening assays for modulators of UCP2 gene
 CC expression, which may be useful for treating disorders in which the UCP2
 CC gene is upregulated in response to fat feeding, e.g. diabetes and obesity

XX

SQ Sequence 736 BP; 119 A; 236 C; 235 G; 146 T; 0 U; 0 Other;

Query Match ... 76.1%; Score 485; DB 2; Length 736;

Best Local Similarity 99.6%; Pred. No. 3.4e-99;

Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```

Qy      129 GGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 188
          |||
Db      1   GGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 60

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Qy      189 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||
Db      61 ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

```



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Qy      249  ACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 308
          |||
Db      120  ACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 179

Qy      309  AGAGAGTGTGAGGCAGAGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
          |||
Db      180  AGAGAGTGTGAGGCAGAGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369  GTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGAGAGAAAGTCATGGAGAGAACCCTA 428
          |||
Db      240  GTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGAGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429  GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||
Db      300  GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489  GGCAGGCCCGGCCCGCCCCGCGAGGCCCAACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 548
          |||
Db      359  GGCAGGCCCGGCCCGCCCCGCGAGGCCCAACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549  CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 608
          |||
Db      419  CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 478

Qy      609  GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479  GTCCACGCTCGCCCGGCTCGTCCGACGCG 507
    
```

RESULT 4

AAV08879

ID AAV08879 standard; cDNA; 736 BP.

XX

AC AAV08879;

XX

DT 20-MAR-2003 (revised)

DT 25-FEB-1999 (first entry)

XX

DE UCP2 promoter.

XX

KW UCP2; promoter; transcription factor; modulator; diabetes; obesity;
KW therapy; ds.

XX

OS Homo sapiens.

XX

PN US5849514-A.

XX

PD 15-DEC-1998.

XX

PF 19-JUN-1998; 98US-00100297.

XX

PR 25-APR-1997; 97US-00846012.

XX

PA (TULA-) TULARIK INC.

XX

PI Chen J, Amaral MC;

XX

DR WPI; 1999-069722/06.

XX

PT Screening assay for modulators of UCP2 gene expression - based on

PT interaction of transcription factor and defined UCP2 promoter sequence.
XX
PS Claim 1; Col 7-8; 9pp; English.
XX
CC This sequence represents the UCP2 promoter, and is used in the method of
CC the invention. The method is a screening assay for agents that modulate
CC the effect of a transcription factor on a UCP2 promoter comprises
CC combining the promoter and transcription factor in the presence and
CC absence of a candidate agent and determining any change in the effect of
CC the transcription factor on the promoter. The promoter comprises at least
CC 50 nucleotides of a sequence comprising nucleotides 1-460 of the UCP2
CC promoter. The method is used to identify agents that modulate UCP2 gene
CC transcription (agents that upregulate UCP2 are potentially useful for
CC treating diabetes and obesity). (Updated on 20-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 736 BP; 119 A; 236 C; 235 G; 146 T; 0 U; 0 Other;

Qy	129	GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG	188
Db	1	GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG	60
Qy	189	ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG	248
Db	61	ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG	119
Qy	249	ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG	308
Db	120	ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG	179
Qy	309	AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA	368
Db	180	AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA	239
Qy	369	GTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAAGTCATGGAGAGAACCCTA	428
Db	240	GTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAAGTCATGGAGAGAACCCTA	299
Qy	429	GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT	488
Db	300	GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T	358
Qy	489	GGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCG	548
Db	359	GGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCG	418
Qy	549	CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT	608
Db	419	CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT	478
Qy	609	GTCCACGCTCGCCCGGCTCGTCCGACGCG	637
Db	479	GTCCACGCTCGCCCGGCTCGTCCGACGCG	507

ID AAV44599 standard; DNA; 1161 BP.
 XX
 AC AAV44599;
 XX
 DT 24-NOV-1998 (first entry)
 XX
 DE Human uncoupling protein-2 UCP2 gene clone hUCP2-g2 sequence 2.
 XX
 KW Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
 KW obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
 KW hypothermia; wasting; cachexia; anorexia; inflammation; fever;
 KW hyperthermia; gene therapy; diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9831396-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 22-APR-1997; 97WO-US006864.
 XX
 PR 15-JAN-1997; 97US-0034960P.
 XX
 PA (UYDU-) UNIV DUKE.
 PA (REGC) UNIV CALIFORNIA.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
 PI Bouillaud F;
 XX
 DR WPI; 1998-413823/35.
 XX
 PT Method for treating disease associated with altered UCP-2 expression - by
 PT administering agent which enhances or inhibits UCP-2 activity,
 PT effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
 PT etc.
 XX
 PS Example II; Fig 10b; 98pp; English.
 XX
 CC This is the nucleotide sequence of a region (sequence 1) of the human
 CC uncoupling protein-2 (UCP2) gene present in genomic clone hUCP2-g2 (I-
 CC 1867). 4 Regions (see V44598-601) of hUCP2-g2 are provided. The hUCP2-g2
 CC clone was isolated from a human placenta genomic DNA library constructed
 CC in lambda EMBL3 phage using a partial genomic fragment as probe. Sequence
 CC 2 corresponds to DNA from positions bp -511 to +650 and includes the
 CC putative proximal human UCP2 promoter. The UCP2 gene maps to a
 CC chromosomal region (11q13) linked to obesity and hyperinsulinaemia. The
 CC invention provides methods for the treatment of disorders associated with
 CC diminished or elevated UCP2 expression or activity. An agent which
 CC enhances UCP2 expression (e.g. an expression construct comprising a UCP2
 CC encoding sequence) can be used to treat obesity, diabetes, syndrome X,
 CC hypothermia, hyperinsulinaemia, or glucose intolerance. An inhibitor of
 CC UCP2 (e.g. an antisense construct) is used to treat wasting, anorexia,
 CC inflammation, cachexia, fever or hyperthermia (all claimed). The
 CC invention also relates to diagnostic and drug screening methodologies
 XX
 SQ Sequence 1161 BP; 209 A; 346 C; 323 G; 234 T; 0 U; 49 Other;

Query Match 70.2%; Score 447.4; DB 2; Length 1161;
 Best Local Similarity 94.9%; Pred. No. 9.5e-91;
 Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

ABL33892

XX

XX

XX

XX

KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW ds.

XX

OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 1865; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 5283 BP; 1097 A; 136 C; 1369 G; 2681 T; 0 U; 0 Other;

Query Match 57.2%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 5.1e-72;
Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

Qy	35	CGACAACGCGGCGGCTGTAACCAATCGACAGCGAGGCCGTCGCGAGGCCCCAGTCCCGC	94
Db	2	CGATAACGCGGCGGTTGTAATTAATCGATAGCGAGGTCGGTCGCGAGGTTTATAGTTTCGT	61
Qy	95	CCTGCAGGAGCCAGCCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGG	154
Db	62	TTTGTAGGAGTTAGTCGCGCGTTCGTTTCGTAGGAGGGTGGGTAGTTGTTTAGCGTA-GG	120
Qy	155	GGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGTTAG	214
Db	121	GGGTTGGGTTTATAAAAGAGGAAGTGTATTTAAGATACGGTTTAG--TGGACGTTGTTAG	178
Qy	215	AAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGT	274
Db	179	AAATCGTTTTGGTTGGGAAGGTAAGAGGTGTGTGATTGGATAAGATTGTTTTTGGCGGT	238
Qy	275	CAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGAG	334
		}	
Db	239	TAGTTTTGTTATTTTTATAGAGGTTGGCGGTTTCGAGAGAGTGTGAGGTAGAGGCGGGGAG	298
Qy	335	TGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGA	394
Db	299	TGGTAAGGGAGTGATTATTTTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGTACGGA	358

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Qy      395 AACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCG 454
          |||
Db      359 AACGGGAGTGGAGAAAGTTATGGAGAGAATTTTAGGCGGGGCGGTTCGCGGAAAGGCG 418

Qy      455 GCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCCGCCCCGCCCCGCAGGC 514
          |||
Db      419 GTTGTTTTAGGGTTTTTCGTATTTAAGTAGGAGTTGGTAGGTTTCGGTTTCGTTTCGTAGGT 478

Qy      515 CCCACCCCGGGCCCCGCCCGAGGCTTAAGCCGCGCCGCGCTGCGCGGAGCCCCACT 574
          |||
Db      479 TTTATTTTCGGGTTTCGTTTTTCGAGGTTTAAGTCGCGTCGTCGTTTTCGCGGAGTTTTATT 538

Qy      575 GCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGAC 634
          |||
Db      539 GCGAAGTTTAGTTGCGCGCGCTTTTGGGATTGATTGTTTACGTTTCGTTTCGGTTCGTTTCGAC 598

Qy      635 GCG 637
          |||
Db      599 GCG 601

```

RESULT 7

ABL33893/c

ID ABL33893 standard; DNA; 5283 BP.

XX

AC ABL33893;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human immune system associated gene SEQ ID NO: 1866.

XX

KW Human; immune system disease; cytosine methylation; antiasthmatic;

KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;

KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;

KW ds.

XX

OS Homo sapiens.

XX

PN WO200200928-A2.

XX

PD 03-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-EP007537.

XX

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-130909/17.

XX

PT Nucleic acid comprising fragment of chemically modified gene, useful for

PT diagnosis and treatment of diseases associated with abnormal cytosine

PT methylation.

```

XX
PS   Claim 1; SEQ ID NO 1866; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention
XX
SQ   Sequence 5283 BP; 1342 A; 136 C; 1475 G; 2330 T; 0 U; 0 Other;

Query Match          49.0%; Score 312.4; DB 6; Length 5283;
Best Local Similarity 72.0%; Pred. No. 2.1e-60;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

Qy      34 CCGACAACGCGGCGGCTGTAACCAATCGACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCG 93
      |||||
Db      5283 CCGACAACGCGACGACTATAACCAATCGACAACGAAACCGATCGCGAAACCCCAATCCCG 5224

Qy      94 CCCTGCAGGAGCCAGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGG 153
      |||||
Db      5223 CCCTACAAAACCAACCGCGCGCTCGCTCGCAAAAAATAAATAATTTACCAACGTA-A 5165

Qy      154 GGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGTTA 213
      |||||
Db      5164 AAAACTAAACCCATAAAAAAAAAAATACACTTAAACACGACCC--AATAACGCTATTA 5107

Qy      214 GAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGG 273
      |||||
Db      5106 AAAACCGTCCTAACTAAAAAACAAAAATATATAACTAAACAAACTTATTTCTAACGA 5047

Qy      274 TCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAGTGTGAGGCAGAGGCGGGGA 333
      |||||
Db      5046 TCAATCTTACCATCCTCACAAAAATTAACGACCCGAAAAAATATAAAACAAAAACGAAAA 4987

Qy      334 GTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGG 393
      |||||
Db      4986 ATAACAAAAAATAACCATCTCGAAAAACGAAAAAATAAACGCGATAATAAACGCACGA 4927

Qy      394 AAACGGGAGTGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGC 453
      |||||
Db      4926 AAACGAAATAAAAAAATCATAAAAAAACCCTAAACGAAACGATCCCCGCGAAAAAAC 4867

Qy      454 GGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCGCAGG 513
      |||||
Db      4866 GACTACTCCAAATCTCCGCACCCAAATAAAACTAACAAACCCGACCCCGCCCGCAAA 4807

Qy      514 CCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCGCGCCTGCGCGGAGCCCCAC 573
      |||||
Db      4806 CCCCACCCCGAACCCCGCCCCGAACTTAAACGCGCCGCGCCTACGCGAAACCCAC 4747

Qy      574 TCGGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGA 633
      |||||
Db      4746 TACGAAACCCAACTACGCGCGCCTTAAATTAATATCCACGCTCGCCGACTCGTCCGA 4687

Qy      634 CGCG 637
      |||||
Db      4686 CGCG 4683

```

RESULT 8

ADP64964

ID ADP64964 standard; DNA; 1646 BP.

XX

AC ADP64964;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human uncoupling protein 2 (mitochondrial, proton carrier) DNA sequence.

XX

KW autoimmune disease; arthritide; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; ds; human.

XX

OS Homo sapiens.

XX

PN WO2003072827-A1.

XX

PD 04-SEP-2003.

XX

PF 31-OCT-2002; 2002WO-US035433.

XX

PR 31-OCT-2001; 2001US-0336220P.

XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX

PI Hirsch R, Thorton SL;

XX

DR WPI; 2003-712740/67.

DR GENBANK; NM_003355.

XX

PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX

PS Disclosure; Page; 56pp; English.

XX

CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for

CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.

XX

SQ Sequence 1646 BP; 309 A; 535 C; 405 G; 397 T; 0 U; 0 Other;

Query Match 10.5%; Score 67; DB 11; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
 |||||
 Db 1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60
 Qy 631 CGACGCG 637
 |||||
 Db 61 CGACGCG 67

RESULT 9

ADJ75174

ID ADJ75174 standard; DNA; 1646 BP.

XX

AC ADJ75174;

XX

DT 20-MAY-2004 (first entry)

XX

DE Marker gene SEQ ID NO:426.

XX

KW bronchial asthma; chronic obstructive pulmonary disease;

KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

KW gene therapy; marker gene; gene; ds.

XX

OS Homo sapiens.

XX

PN EP1394274-A2.

XX

PD 03-MAR-2004.

XX

PF 04-AUG-2003; 2003EP-00254857.

XX

PR 06-AUG-2002; 2002JP-00229312.

PR 20-MAR-2003; 2003JP-00077212.

XX

PA (GENO-) GENOX RES INC.

XX

PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX

DR WPI; 2004-193155/19.

XX

PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX

PS Claim 1; SEQ ID NO 426; 241pp; English.

XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX
 SQ Sequence 1646 BP; 309 A; 535 C; 405 G; 397 T; 0 U; 0 Other;

Query Match 10.5%; Score 67; DB 12; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60
 QY 631 CGACGCG 637
 |||||
 Db 61 CGACGCG 67

RESULT 10

ADY16091

ID ADY16091 standard; DNA; 1646 BP.

XX

AC ADY16091;

XX

DT 05-MAY-2005 (first entry)

XX

DE DNA encoding a PRO polypeptide, SEQ ID NO 1897.

XX

KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;

KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;

KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

KW Antiallergic; ds; gene; diagnosis.

XX
 OS Homo sapiens.
 XX
 PN WO2005016962-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 11-AUG-2004; 2004WO-US026249.
 XX
 PR 11-AUG-2003; 2003US-0493546P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
 XX
 DR WPI; 2005-182330/19.
 XX
 PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
 XX
 PS Claim 1; SEQ ID NO 1897; 158pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a DNA encoding a PRO
 CC polypeptide.
 XX
 SQ Sequence 1646 BP; 309 A; 535 C; 405 G; 397 T; 0 U; 0 Other;

Query Match 10.5%; Score 67; DB 14; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

 Qy 631 CGACGCG 637
 |||||
 Db 61 CGACGCG 67

RESULT 11

ADP65417

ID ADP65417 standard; DNA; 8177 BP.

XX

AC ADP65417;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human uncoupling protein-2 (UCP2) gene, nuclear gene DNA.

XX

KW autoimmune disease; arthritide; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; ds; human.

XX
 OS Homo sapiens.
 XX
 PN WO2003072827-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Hirsch R, Thorton SL;
 XX
 DR WPI; 2003-712740/67.
 DR GENBANK; AF096289.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX
 SQ Sequence 8177 BP; 1708 A; 2261 C; 2020 G; 2188 T; 0 U; 0 Other;

Query Match 10.5%; Score 67; DB 11; Length 8177;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

Qy 631 CGACGCG 637
 |||||
 Db 61 CGACGCG 67

RESULT 12

AAS94928

ID AAS94928 standard; DNA; 1643 BP.

XX

AC AAS94928;

XX

DT 14-FEB-2002 (first entry)

XX

DE Human DNA sequence #183 expressed during foam cell differentiation.

XX

KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;

KW cardiovascular disorder; coronary artery disease; gene therapy; ds.

XX

OS Homo sapiens.

XX

PN WO200177389-A2.

XX

PD 18-OCT-2001.

XX

PF 04-APR-2001; 2001WO-US011128.

XX

PR 05-APR-2000; 2000US-0195106P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;

PI Tai J;

XX

DR WPI; 2002-010925/01.

XX

PT Composition useful for diagnosis of conditions, disorders or diseases

PT associated with atherosclerosis, comprises several polynucleotides that

PT are differentially expressed in foam cell development.

XX

PS Claim 1; Page 238; 315pp; English.

XX

CC The present invention relates to the isolation of human polynucleotide

CC sequences that are differentially expressed during foam cell

CC differentiation. The polynucleotide sequences of the invention or a

CC composition comprising these polynucleotides are useful as a high

CC throughput method for detecting altered expression of one or more

CC polynucleotides in a sample. The polynucleotides can be used in the

CC diagnosis of disorders associated with foam cell development such as

CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as

CC coronary artery disease. The polynucleotide sequences can also be used as

CC PCR primers and probes. The polynucleotides of the invention are also

CC useful in gene therapy. AAS94746-AAS95021 represent the human

CC polynucleotide sequences of the invention which are differentially

CC expressed during foam cell differentiation

XX

SQ Sequence 1643 BP; 311 A; 533 C; 402 G; 397 T; 0 U; 0 Other;

Query Match 9.1%; Score 58; DB 6; Length 1643;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 GCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
 |||
 Db 1 GCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 58

RESULT 13

AAC10386

ID AAC10386 standard; cDNA; 161 BP.

XX

AC AAC10386;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 14461.

XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX

OS Homo sapiens.

XX

PN EP1033401-A2.

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX

DR WPI; 2000-500381/45.

XX

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX

PS Claim 1; SEQ ID NO 14461; 71pp + Sequence Listing; English.

XX

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors

XX

SQ Sequence 161 BP; 25 A; 64 C; 41 G; 30 T; 0 U; 1 Other;

Query Match 8.9%; Score 57; DB 3; Length 161;

Best Local Similarity 96.6%; Pred. No. 0.0026;

Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

ID ADB87421 standard; DNA; 2500 BP.

XX

AC ADB87421;

XX

DT 04-DEC-2003 (first entry)

XX

DE Transgene expression regulatory element, STAR66F.

XX

KW gene transcription; regulatory; variety fragment; STAR element;

KW transgene expression; ds.

XX

OS Unidentified.

XX

PN WO2003004704-A2.

XX

PD 16-JAN-2003.

XX

PF 14-JUN-2002: 2002WO-NL000390.

XX

PR 04-JUL-2001; 2001EP-00202581.

PR 05-JUL-2001; 2001US-0303199P.

XX

PA (CHRO-) CHROMAGENICS BV.

XX

PI Otte AP, Kruckeberg AL;

XX

DR WPI: 2003-229412/22.

XX

PT Selecting a DNA sequence with a gene transcription modulating quality by
PT providing a transcription system with a variety fragment-comprising
PT vectors and performing a selection step in the transcription system.

XX

PS Claim 43; Fig 26; 216pp; English.

XX

CC The invention relates to DNA sequences with gene transcription regulatory
CC qualities and methods for the detection and use of the regulatory DNA
CC sequences. The invention further comprises providing a transcription
CC system with a variety fragment-comprising vectors; and performing a
CC selection step in the transcription system in order to identify a
CC fragment comprising the DNA sequence with the gene transcription
CC modulating activity. This polynucleotide represents a STAR element used
CC in the method of the invention. The STAR element is shown to improve
CC transgene expression.

XX

Sequence 2500 BP; 295 A; 902 C; 981 G; 322 T; 0 U; 0 Other;

Query Match 8.1%; Score 51.8; DB 10; Length 2500;

Best Local Similarity 52.0%; Pred. No. 0.052;

Matches 116; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 374 CGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAAGTCATGGAGAGAACCCTAGGCGG 433
 ||| || | ||| | || | ||| ||| | |||
 Db 1156 CGCGCGCCGGGACGGGACGGGACGGGGCGGGCGGGGCGGGACGAGACGGGGCGGGGCGG 1215

```

QY      434  GCGGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAG 493
          ||||| || || |      ||| || | | | | || || | | | |
Db      1216  GCGGGGCCGGGCAGCCTCCGGGCGGCGCGGGCGGGCGGGCCGGATCCAGGGCGGGGG 1275

QY      494  GCGCGGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGCTTAAGCCGCGCCG 553
          | | |||| || || | ||| ||||| || | ||| || | |||||
Db      1276  TCGGCGGCCCGGCCAGCCCGGCCCGGGCCGGGCGCGTCTGAGAGTCAGCCCTCGCCG 1335

QY      554  CCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCC 596
          | || | ||| |||| | | ||| | |||| | ||
Db      1336  CTGCAGCCTCGGCGCCCGGCCGGCCGGCCATGGAGCGCCCCC 1378
  
```

RESULT 15

ADJ35230

ID ADJ35230 standard; DNA; 2500 BP.

XX

AC ADJ35230;

XX

DT 22-APR-2004 (first entry)

XX

DE Human stabilising anti-repression, STAR, element #66.

XX

KW STAR affiliated proteinaceous molecule; post translational modification;

KW human; stabilising anti-repression; STAR; STAR element; ds.

XX

OS Homo sapiens.

XX

PN WO2003106674-A2.

XX

PD 24-DEC-2003.

XX

PF 30-MAY-2003; 2003WO-NL000410.

XX

PR 14-JUN-2002; 2002EP-00077344.

XX

PA (CHRO-) CHROMAGENICS BV.

XX

PI Otte AP, Kruckeberg AL, Satijn DPE;

XX

DR WPI; 2004-082195/08.

XX

PT Producing proteinaceous molecules in cells by selecting a cell, providing

PT a nucleic acid encoding a proteinaceous molecule with an STabilizing Anti

PT -Repression sequence and expressing proteinaceous molecule.

XX

PS Example 1; SEQ ID NO 66; 177pp; English.

XX

CC The invention relates to a method of producing a proteinaceous molecule

CC (I) in a cell comprising selecting a cell for its suitability for

CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid

CC comprising a STabilising Anti-Repression (STAR) sequence, expressing the

CC resulting nucleic acid in the cell and collecting (I). The method is

CC useful for producing (I). A cell line (II) provided with a nucleic acid

CC comprising a STAR sequence is useful for producing (I). (II) Enables

CC production of affiliated proteinaceous molecule, as cell carries out

CC proper post-translational modifications of produced proteins. The present

CC sequence represents a human stabilising anti-repression, STAR, element.

XX

SQ Sequence 2500 BP; 295 A; 903 C; 980 G; 322 T; 0 U; 0 Other;

Query Match 8.1%; Score 51.8; DB 12; Length 2500;
Best Local Similarity 52.0%; Pred. No. 0.052;
Matches 116; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

```
Qy      374 CGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGAGAACCCCTAGGCGG 433
      ||||  ||  | |||| | ||| | |||  ||||  | ||||
Db      1156 CGCGGCCCGGGACGGGACGGGACGGGGCGGGCGGGGCGGGACGAGACGGGGCGGGGCGG 1215

Qy      434 GCGGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAG 493
      |||| | || | || | || | || | || | || | || | || |
Db      1216 GCGGGGCCGGGCAGCCTCCGGGCGGGCGGGCGGGCGGGCGGGCGGCCGGATCCAGGGCGGGGG 1275

Qy      494 GCGGGGCCCGGGCGGGCGAGGGCCCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGG 553
      | | |||| || || | || | |||| || | || || | || || || ||
Db      1276 TCGGGCGGGCCGGCCAGCCCGGGCCCGGGCGGGGGCGGGCGGGCGGGCGGGCGGGCGGG 1335

Qy      554 CCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGGCC 596
      || | || || || || | | || | || || || ||
Db      1336 CTGCAGCCTCGGGCGCCCGGGCCGGCCGGCCATGGAGCGCCCCCC 1378
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Job time : 552 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09869098 and Search Result us-09-869-098a-1_copy_1634_2270.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09869098 and Search Result us-09-869-098a-1_copy_1634_2270.rge.

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OM nucleic - nucleic search, using sw model

Run on: June 6, 2006, 20:07:49 ; Search time 4056 Seconds
(without alignments)
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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
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1	637	100.0	3505	2	E54511	E54511 UCP-2 promo
2	625	98.1	12177	5	DQ087219	DQ087219 Homo sapi
c 3	625	98.1	156370	5	AP003717	AP003717 Homo sapi
c 4	625	98.1	199384	5	AP003531	AP003531 Homo sapi
5	623.4	97.9	3270	5	AF306570	AF306570 Homo sapi
6	599.8	94.2	197031	12	AC019121	AC019121 Homo sapi
c 7	599.4	94.1	155668	12	AC024029	AC024029 Homo sapi
8	519	81.5	2131	5	AK025742	AK025742 Homo sapi
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10	485	76.1	736	2	AR065267	AR065267 Sequence
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12	481.4	75.6	3301	5	AF208500	AF208500 Homo sapi
13	364.2	57.2	5283	2	AX346794	AX346794 Sequence
c 14	312.4	49.0	5283	2	AX346795	AX346795 Sequence
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16	67	10.5	1646	2	CS032391	CS032391 Sequence
17	67	10.5	1646	2	CS041343	CS041343 Sequence
18	67	10.5	8177	5	AF096289	AF096289 Homo sapi
19	66	10.4	1618	5	AK222540	AK222540 Homo sapi
20	66	10.4	1679	5	AK222557	AK222557 Homo sapi
c 21	60	9.4	7218	2	I66494	I66494 Sequence 14
22	58	9.1	1643	2	AX281774	AX281774 Sequence
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c 26	55.4	8.7	202971	12	CR759948	CR759948 Danio rer
27	55	8.6	182060	12	AC145822	AC145822 Pan trogl
28	54.2	8.5	972	7	PM12A12G	AL684288 Penicilli
c 29	54	8.5	976	7	PM12D6G	AL684370 Penicilli
30	53	8.3	61676	12	AC060800	AC060800 Homo sapi
c 31	52.6	8.3	125020	5	AF429315	AF429315 Homo sapi
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34	51.8	8.1	2500	2	CQ755565	CQ755565 Sequence
35	51.8	8.1	2500	2	CQ757762	CQ757762 Sequence
36	51.8	8.1	2500	2	CS208903	CS208903 Sequence
37	51.8	8.1	2500	2	AX764596	AX764596 Sequence
38	51.8	8.1	120917	5	HSJ583P15	AL121845 Human DNA
39	51.6	8.1	257047	12	AC090879	AC090879 Mus muscu
40	51.2	8.0	991	7	PM12H12B	AL684455 Penicilli
c 41	51.2	8.0	159028	12	AC142003	AC142003 Rattus no
c 42	51	8.0	1401	2	AR763821	AR763821 Sequence
c 43	51	8.0	156500	12	CR792441	CR792441 Danio rer
44	50.8	8.0	10732	2	E32986	E32986 Gene encodi
c 45	50.8	8.0	96895	12	AC141768	AC141768 Apis mell

ALIGNMENTS

RESULT 1
E54511

LOCUS E54511 3505 bp DNA linear PAT 31-JAN-2002
 DEFINITION UCP-2 promoter and use thereof.
 ACCESSION E54511
 VERSION E54511.1 GI:18629692
 KEYWORDS JP 2000236886-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3505)
 AUTHORS Toyota,Y., Kobayashi,M. and Igaki,S.
 TITLE UCP-2 promoter and use thereof
 JOURNAL Patent: JP 2000236886-A 1 05-SEP-2000;
 TAKEDA CHEM IND LTD
 COMMENT OS Homo sapiens (human)
 PN JP 2000236886-A/1
 PD 05-SEP-2000
 PF 22-DEC-1999 JP 1999364724
 PR
 PI YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
 PC C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P3/10, A61P9/12, PC
 A61P29/00, C12N1/21,
 PC C12N5/10, C12Q1/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,
 PC A61K48/00,
 PC (C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
 PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
 PC C12R1:19),
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 FT source 1. .3505
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ORIGIN

Query Match 100.0%; Score 637; DB 2; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 1.8e-169;
 Matches 637; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ACCTGTTGCTGCAGTTCTGATTGGTTCCCTTCCCCGACAACGCGGCGGCTGTAACCAATC  60
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Qy      61  GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
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Db      1694 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 1753

Qy      121 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGGCCATAAAAGAGGAAGTG 180
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Qy      181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
      |||
Db      1814 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 1873

Qy      241 GGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 300
  
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|||||
Db      1874 GGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 1933
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Db      1934 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 1993
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QY      421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
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QY      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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Db      2234 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 2270

```

RESULT 2

DQ087219

LOCUS DQ087219 12177 bp DNA linear PRI 18-JUN-2005

DEFINITION Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier) (UCP2) gene, complete cds; nuclear gene for mitochondrial product.

ACCESSION DQ087219

VERSION DQ087219.1 GI:67515418

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 12177)

AUTHORS Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Baier,C.N., Rajkumar,N., Willa,H.T., Daniels,M., Downing,T.K., Stanaway,I.B., Nguyen,C.P., Gildersleeve,H., Cassidy,C.M., Johnson,E.J., Swanson,J.E., McFarland,I., Yool,B., Park,C. and Nickerson,D.A.

TITLE Direct Submission

JOURNAL Submitted (07-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA

COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).

FEATURES Location/Qualifiers

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	/frequency="0.03"
	/replace="t"
gene	2001. .10177
	/gene="UCP2"
mRNA	join(2001. .2124,3213. .3369,6369. .6593,6750. .6960,7829. .8023,8104. .8205,9175. .9355,9727. .10177)
	/gene="UCP2"
	/product="uncoupling protein 2 (mitochondrial, proton carrier)"
variation	2052
	/gene="UCP2"
	/frequency="0.04"
	/replace="t"
variation	2089
	/gene="UCP2"
	/frequency="0.06"
	/replace="g"
repeat_region	2242. .2540
	/rpt_family="Alu"
	/rpt_type=dispersed
variation	2469
	/gene="UCP2"
	/frequency="0.48"
	/replace="c"
variation	2818
	/gene="UCP2"
	/frequency="0.02"
	/replace="t"
variation	2900
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	/frequency="0.06"
	/replace="t"
variation	3310
	/gene="UCP2"
	/frequency="0.05"
	/replace="t"
variation	3473
	/gene="UCP2"
	/frequency="0.07"
	/replace="g"
repeat_region	3574. .3699
	/rpt_family="MIR"
	/rpt_type=dispersed
variation	3856
	/gene="UCP2"
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	/replace=""

variation	3957 /gene="UCP2" /frequency="0.02" /replace="g"
variation	3999 /gene="UCP2" /frequency="0.02" /replace="a"
variation	4047 /gene="UCP2" /frequency="0.01" /replace="g"
variation	4117 /gene="UCP2" /frequency="0.10" /replace="g"
repeat_region	4180. .4254 /rpt_family="MIR" /rpt_type=dispersed
misc_feature	4388. .5633 /gene="UCP2" /note="Region not scanned for variation"
repeat_region	5001. .5272 /rpt_family="Alu" /rpt_type=dispersed
repeat_region	5273. .5581 /rpt_family="Alu" /rpt_type=dispersed
variation	5955 /gene="UCP2" /frequency="0.02" /replace="g"
variation	5972 /gene="UCP2" /frequency="0.01" /replace="a"
variation	6328 /gene="UCP2" /frequency="0.01" /replace="a"
variation	6374 /gene="UCP2" /frequency="0.01" /replace="a"
CDS	join(6468. .6593,6750. .6960,7829. .8023,8104. .8205, 9175. .9355,9727. .9841) /gene="UCP2" /codon_start=1 /product="uncoupling protein 2 (mitochondrial, proton carrier)" /protein_id="AAY68217.1" /db_xref="GI:67515419" /translation="MVGFKATDVPPTATVKFLGAGTAACIADLITFPLDTAKVRLQIQ GESQGPVRATASAQYRGVMGTILTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLYDS VKQFYTKGSEHASIGSRLLAGSTTGALAVAVAQPTDVVKVRFQAQARAGGGRRYQSTV NAYKTIAREEGFRGLWKGTSFNVARNAINCAELVITYDLIKDALLKANLMTDDLPCHE TSAFGAGFCTTVIASPVDVVKTRYMNSALGQYSSAGHCALTMLQKEGPRAFYKGFMP FLRLGSWNVVMFVITYEQLKRALMAACTSREAPF"
variation	6779 /gene="UCP2" /frequency="0.01"

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variation      /replace="t"
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                /frequency="0.46"
                /replace="t"
variation      6850
                /gene="UCP2"
                /frequency="0.02"
                /replace="a"
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                /rpt_type=dispersed
variation      7357
                /gene="UCP2"
                /frequency="0.02"
                /replace=""
repeat_region  7361. .7480
                /rpt_family="MIR"
                /rpt_type=dispersed
variation      7435
                /gene="UCP2"
                /frequency="0.01"
                /replace="c"
repeat_region  7486. .7570
                /rpt_family="MIR"
                /rpt_type=dispersed
variation      7566
                /gene="UCP2"
                /frequency="0.02"
                /replace="g"
variation      7723
                /gene="UCP2"
                /frequency="0.07"
                /replace="a"
variation      7747
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                /frequency="0.02"
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variation      7794
                /gene="UCP2"
                /frequency="0.01"
                /replace="a"
variation      7804
                /gene="UCP2"
                /frequency="0.01"
                /replace="t"
variation      7952
    
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Query Match 98.1%; Score 625; DB 5; Length 12177;
 Best Local Similarity 99.8%; Pred. No. 5.3e-166;
 Matches 636; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1  ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGGCGGCTGTAACCAATC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1432 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGGCGGCTGTAACCAATC 1491

Qy      61  GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1492 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 1551

Qy      121 TCGCAGGAGGGTGGGTAGTTTGCCGACGCTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
    
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Db      1552 TCGCAGGAGGGTGGGTAGTTTGCCACGCTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 1611
Qy      181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
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Db      1612 CACTTAAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 1670
Qy      241 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 300
|||||
Db      1671 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 1730
Qy      301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 360
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Db      1731 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 1790
Qy      361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAAAGTCATGGAGA 420
|||||
Db      1791 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAAAGTCATGGAGA 1850
Qy      421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
|||||
Db      1851 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 1910
Qy      481 TAGGAGCTGGCAGGCCCGGCCCCGCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 540
|||||
Db      1911 TAGGAGCTGGCAGGCCCGGCCCCGCGCAGGCCCCACCCCGGGCCCCGCCCCGAGGC 1970
Qy      541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
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Db      1971 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 2030
Qy      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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RESULT 3

AP003717/c

LOCUS AP003717 156370 bp DNA linear PRI 27-APR-2002

DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete sequences.

ACCESSION AP003717

VERSION AP003717.3 GI:20334343

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens genomic DNA

JOURNAL Published Only in Database (2001)

REFERENCE 2 (bases 1 to 156370)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:16904692.
FEATURES Location/Qualifiers
source 1. .156370
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-167N4"

ORIGIN

Query Match 98.1%; Score 625; DB 5; Length 156370;
Best Local Similarity 99.8%; Pred. No. 6.9e-166;
Matches 636; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGCGGCTGTAACCAATC 60
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Db 43495 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTCCCCGACAACGCGGCGGCTGTAACCAATC 43436

Qy      61 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
      |||
Db 43435 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 43376

Qy     121 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
      |||
Db 43375 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 43316

Qy     181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
      |||
Db 43315 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 43257

Qy     241 GGTGTGTGACTGGACAAGACTTGT TTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 300
      |||
Db 43256 GGTGTGTGACTGGACAAGACTTGT TTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 43197

Qy     301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 360
      |||
Db 43196 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 43137

Qy     361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 420
      |||
Db 43136 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 43077

Qy     421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
      |||
Db 43076 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 43017

Qy     481 TAGGAGCTGGCAGGCCCGGCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGC 540
      |||
Db 43016 TAGGAGCTGGCAGGCCCGGCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGC 42957

Qy     541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
      |||
Db 42956 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 42897

Qy     601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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Db 42896 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 42860
    
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RESULT 4
AP003531/c
LOCUS AP003531 199384 bp DNA linear PRI 27-APR-2002
DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-535C12,
complete sequences.
ACCESSION AP003531
VERSION AP003531.2 GI:20334341
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 199384)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:13699094.
FEATURES Location/Qualifiers
source 1. .199384
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-535C12"

ORIGIN

Query Match 98.1%; Score 625; DB 5; Length 199384;
Best Local Similarity 99.8%; Pred. No. 7e-166;
Matches 636; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1  ACCTGTTGCTGCAGTTCTGATTGGTTCCCTTCCCCGACAACGCGGCGGCTGTAACCAATC  60
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Qy      61  GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
          |||
Db    180976 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCCCGCCCTGCAGGAGCCAGCCGCGCGCTCGC 180917

Qy     121  TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
          |||
Db    180916 TCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180857

Qy     181  CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
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Db    180856 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 180798

Qy     241  GGTGTGTGACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 300
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Db      180797 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 180738
QY      301 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 360
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Db      180737 GCGGCCCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGA 180678
QY      361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 420
        |||
Db      180677 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGGAGAAAGTCATGGAGA 180618
QY      421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
        |||
Db      180617 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 180558
QY      481 TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCGGAGGC 540
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Db      180557 TAGGAGCTGGCAGGCCCGGCCCGCCCCGCAGGCCCCACCCCGGGCCCCGCCCGGAGGC 180498
QY      541 TTAAGCCGCGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
        |||
Db      180497 TTAAGCCGCGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 180438
QY      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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RESULT 5

AF306570

LOCUS AF306570 3270 bp DNA linear PRI 30-OCT-2000

DEFINITION Homo sapiens uncoupling protein 2 gene, promoter region and exon 1; nuclear gene for mitochondrial product.

ACCESSION AF306570

VERSION AF306570.1 GI:11037742

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 3270)

AUTHORS Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.

TITLE UCP2 promoter region and exon 1

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3270)

AUTHORS Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.

TITLE Direct Submission

JOURNAL Submitted (18-SEP-2000) Laboratory Medicine, Landeskliniken
Salzburg, Muellner Hauptstr. 48, Salzburg A-5020, Austria

FEATURES Location/Qualifiers

source

1. .3270

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q13"

promoter

1. .3117

mRNA

3118. .>3241

/product="uncoupling protein 2"

/note="UCP2"

exon

3118. .3241

/number=1

ORIGIN

Query Match 97.9%; Score 623.4; DB 5; Length 3270;
 Best Local Similarity 99.7%; Pred. No. 1.3e-165;
 Matches 635; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      61 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
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Db      2609 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 2668

Qy      121 TCGCAGGAGGGTGGGTAGTTTGCCACGCTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
        |||
Db      2669 TCGCAGGAGGGTGGGTAGTTTGCCACGCTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 2728

Qy      181 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
        |||
Db      2729 CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 2787

Qy      241 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 300
        |||
Db      2788 GGTGTGTGACTGGACAAGACTTGTCTTCTGGCGGTCAGTCTTGCCATCTCACAGAGGTTG 2847

Qy      301 GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 360
        |||
Db      2848 GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGA 2907

Qy      361 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGAGAGAAAGTCATGGAGA 420
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Db      2908 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTGAGAGAAAGTCATGGAGA 2967

Qy      421 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
        |||
Db      2968 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 3027

Qy      481 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGGCCCCGCCCCGAGGC 540
        |||
Db      3028 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGGCCCCCTCCCCGAGGC 3087

Qy      541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
        |||
Db      3088 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 3147

Qy      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
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Db      3148 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 3184
  
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RESULT 6

AC019121

LOCUS AC019121 197031 bp DNA linear HTG 07-JUL-2000

DEFINITION Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT
SEQUENCE, 23 unordered pieces.

ACCESSION AC019121

VERSION AC019121.3 GI:8440022

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 197031)
 AUTHORS Waterston,R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 197031)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT On Jun 10, 2000 this sequence version replaced gi:7105573.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site:<http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----
 Center project name: H_NH0535C12

----- Summary Statistics -----
 Sequencing vector: M13; 55%
 Sequencing vector: plasmid; 45%
 Chemistry: Dye-primer ET; 55% of reads
 Chemistry: Dye-terminator Big Dye; 45% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 182418 bases at least Q40
 Consensus quality: 187565 bases at least Q30
 Consensus quality: 190012 bases at least Q20
 Insert size: 190000; agarose-fp
 Insert size: 194831; sum-of-contigs
 Quality coverage: 4.10 in Q20 bases; agarose-fp
 Quality coverage: 4.05 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 23 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2971: contig of 2971 bp in length
 * 2972 3071: gap of unknown length
 * 3072 5764: contig of 2693 bp in length
 * 5765 5864: gap of unknown length
 * 5865 8568: contig of 2704 bp in length
 * 8569 8668: gap of unknown length
 * 8669 12865: contig of 4197 bp in length
 * 12866 12965: gap of unknown length
 * 12966 18581: contig of 5616 bp in length
 * 18582 18681: gap of unknown length
 * 18682 23851: contig of 5170 bp in length
 * 23852 23951: gap of unknown length
 * 23952 28414: contig of 4463 bp in length
 * 28415 28514: gap of unknown length
 * 28515 33195: contig of 4681 bp in length
 * 33196 33295: gap of unknown length
 * 33296 38648: contig of 5353 bp in length

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* 38649 38748: gap of unknown length
* 38749 44925: contig of 6177 bp in length
* 44926 45025: gap of unknown length
* 45026 51784: contig of 6759 bp in length
* 51785 51884: gap of unknown length
* 51885 58855: contig of 6971 bp in length
* 58856 58955: gap of unknown length
* 58956 68289: contig of 9334 bp in length
* 68290 68389: gap of unknown length
* 68390 77123: contig of 8734 bp in length
* 77124 77223: gap of unknown length
* 77224 87292: contig of 10069 bp in length
* 87293 87392: gap of unknown length
* 87393 96029: contig of 8637 bp in length
* 96030 96129: gap of unknown length
* 96130 104791: contig of 8662 bp in length
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* 104892 116912: contig of 12021 bp in length
* 116913 117012: gap of unknown length
* 117013 131368: contig of 14356 bp in length
* 131369 131468: gap of unknown length
* 131469 142993: contig of 11525 bp in length
* 142994 143093: gap of unknown length
* 143094 154361: contig of 11268 bp in length
* 154362 154461: gap of unknown length
* 154462 173802: contig of 19341 bp in length
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* 173903 197031: contig of 23129 bp in length.

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FEATURES	Location/Qualifiers
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gap	2972. .3071 /estimated_length=unknown
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misc_feature	33296. .38648 /note="assembly_name:Contig34"
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misc_feature	38749. .44925 /note="assembly_name:Contig35"
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misc_feature	45026. .51784 /note="assembly_name:Contig36"
gap	51785. .51884 /estimated_length=unknown
misc_feature	51885. .58855 /note="assembly_name:Contig37"
gap	58856. .58955 /estimated_length=unknown
misc_feature	58956. .68289 /note="assembly_name:Contig38"
gap	68290. .68389 /estimated_length=unknown
misc_feature	68390. .77123 /note="assembly_name:Contig39"
gap	77124. .77223 /estimated_length=unknown
misc_feature	77224. .87292 /note="assembly_name:Contig40"
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misc_feature	96130. .104791 /note="assembly_name:Contig42"
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misc_feature	143094. .154361 /note="assembly_name:Contig46 clone_end:T7 vector_side:left"
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Query Match 94.2%; Score 599.8; DB 12; Length 197031;
Best Local Similarity 98.4%; Pred. No. 1e-158;
Matches 627; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

RESULT 7
AC024029/c
LOCUS AC024029 155668 bp DNA linear HTG 07-JUL-2000

DEFINITION Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
ACCESSION AC024029
VERSION AC024029.3 GI:7230916
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:<http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----
Center project name: H_NH0167N04

----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	1806: contig of 1806 bp in length
*	1807	1906: gap of unknown length
*	1907	4798: contig of 2892 bp in length
*	4799	4898: gap of unknown length
*	4899	7312: contig of 2414 bp in length
*	7313	7412: gap of unknown length
*	7413	11277: contig of 3865 bp in length
*	11278	11377: gap of unknown length
*	11378	14368: contig of 2991 bp in length
*	14369	14468: gap of unknown length
*	14469	20130: contig of 5662 bp in length

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*      20131      20230: gap of unknown length
*      20231      25513: contig of 5283 bp in length
*      25514      25613: gap of unknown length
*      25614      30765: contig of 5152 bp in length
*      30766      30865: gap of unknown length
*      30866      37337: contig of 6472 bp in length
*      37338      37437: gap of unknown length
*      37438      45571: contig of 8134 bp in length
*      45572      45671: gap of unknown length
*      45672      60199: contig of 14528 bp in length
*      60200      60299: gap of unknown length
*      60300      71424: contig of 11125 bp in length
*      71425      71524: gap of unknown length
*      71525      86218: contig of 14694 bp in length
*      86219      86318: gap of unknown length
*      86319     104104: contig of 17786 bp in length
*     104105     104204: gap of unknown length
*     104205     155668: contig of 51464 bp in length.

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FEATURES      Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="11"
                /clone="RP11-167N4"
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                /note="assembly_name:Contig13"
gap            1807. .1906
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gap            4799. .4898
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misc_feature    4899. .7312
                /note="assembly_name:Contig15"
gap            7313. .7412
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misc_feature    7413. .11277
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gap            11278. .11377
                /estimated_length=unknown
misc_feature    11378. .14368
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                clone_end:SP6
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gap            14369. .14468
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                /estimated_length=unknown
misc_feature    20231. .25513
                /note="assembly_name:Contig19"
gap            25514. .25613
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misc_feature    25614. .30765
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gap          60200. .60299
              /estimated_length=unknown
misc_feature 60300. .71424
              /note="assembly_name:Contig24"
gap          71425. .71524
              /estimated_length=unknown
misc_feature 71525. .86218
              /note="assembly_name:Contig25
              clone_end:T7
              vector_side:right"
gap          86219. .86318
              /estimated_length=unknown
misc_feature 86319. .104104
              /note="assembly_name:Contig26"
gap          104105. .104204
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misc_feature 104205. .155668
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ORIGIN

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Query Match          94.1%; Score 599.4; DB 12; Length 155668;
Best Local Similarity 99.4%; Pred. No. 1.3e-158;
Matches 633; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
    
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Qy      1  ACCTGTTGCTGCAGTTCTGATTGGTTCCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 60
          |||
Db      68782 ACCTGTTGCTGCAGTTCTGATTGGTTCCCTTCCCCGACAACGCGGCGGCTGTAACCAATC 68723

Qy      61  GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 120
          |||
Db      68722 GACAGCGAGGCCGGTCGCGAGGCCCCAGTCCC GCCCTGCAGGAGCCAGCCGCGCGCTCGC 68663

Qy      121  TCGCAGGAGGGTGGGTAGTTT GCCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 180
          |||
Db      68662 TCGCAGGAGGGTGGGTAGTTT GCCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTG 68603

Qy      181  CACTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 240
          |||
Db      68602 CACTTAAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGA 68544

Qy      241  GGTGTGTGACTGGACAAGACTTGT TTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 300
          |||
Db      68543 GGTGTGTGACTGGACAAGACTTGT TTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTG 68484

Qy      301  GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTG GCAAGGGAGTGACCATCTCGGGGA 360
          |||
Db      68483 GCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAGTG GCAAGGGAGTGACCATCTCGGGGA 68424

Qy      361  ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTG GAGAAAGTCATGGAGA 420
          |||
Db      68423 ACGAAGGAGTAAACGCGGTGATGGGACGCACGGAAACGGGAGTG GAGAAAGTCATGGAGA 68364

Qy      421  GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 480
    
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Db      68363 GAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAG 68304
QY      481 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGAGGCCCCACCCGGGCCCCGCCCCGAGGC 540
|||||
Db      68303 TAGGAGCTGGCAGGCCCGGCCCCGCCCCGCATGCCCCACCCGGGCCCCGCCCCGAGGC 68244
QY      541 TTAAGCCGCGCCGCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 600
|||||
Db      68243 TTAAG-CGCGCCGCGCCTGCGC-GAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGG 68186
QY      601 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 637
|||||
Db      68185 GATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG 68149

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RESULT 8

AK025742

LOCUS AK025742 2131 bp mRNA linear PRI 13-SEP-2003

DEFINITION Homo sapiens cDNA: FLJ22089 fis, clone HEP16080, highly similar to HSU94592 Human uncoupling protein homolog (UCPH) mRNA.

ACCESSION AK025742

VERSION AK025742.1 GI:10438354

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1

AUTHORS

Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2131)

AUTHORS

Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES

source

Location/Qualifiers

1. .2131

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HEP16080"

/cell_line="HepG2"

/cell_type="hepatoma"

/clone_lib="HEP"

/note="cloning vector pME18SFL3"

misc_feature 1. .2131
/note="highly similar to HSU94592 Human uncoupling protein
homolog (UCPH) mRNA"

ORIGIN

Query Match 81.5%; Score 519; DB 5; Length 2131;
Best Local Similarity 99.8%; Pred. No. 6e-136;
Matches 530; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	107	AGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGCTGGGCCCCA	166
Db	1	AGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGGGGCTGGGCCCCA	60
Qy	167	TAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGG	226
Db	61	TAAAAGAGGAAGTGCACCTTAAGACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGG	119
Qy	227	CTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCAT	286
Db	120	CTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCAT	179
Qy	287	CCTCACAGAGGTTGGCGGCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGT	346
Db	180	CCTCACAGAGGTTGGCGGCCGAGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGT	239
Qy	347	GACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGA	406
Db	240	GACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGA	299
Qy	407	GAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGG	466
Db	300	GAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGG	359
Qy	467	TCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGCCCCGCCCCGAGGCCCCACCCCGGGC	526
Db	360	TCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGCCCCGCCCCGAGGCCCCACCCCGGGC	419
Qy	527	CCCGCCCCCGAGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGC	586
Db	420	CCCGCCCCCGAGGCTTAAGCCGCGCCGCCGCTGCGCGGAGCCCCACTGCGAAGCCCAGC	479
Qy	587	TGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG	637
Db	480	TGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGACGCG	530

RESULT 9

AR039137

LOCUS	AR039137	736 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 1 from patent US 5807740.				
ACCESSION	AR039137				
VERSION	AR039137.1 GI:5958500				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 736)				
AUTHORS	Amaral,M.Catherine. and Chen,J.-L.				
TITLE	Regulators of UCP2 gene expression				
JOURNAL	Patent: US 5807740-A 1 15-SEP-1998;				
FEATURES	Location/Qualifiers				

source 1. .736
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 76.1%; Score 485; DB 2; Length 736;
Best Local Similarity 99.6%; Pred. No. 2.5e-126;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy      129 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 188
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Db      1   GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 60

Qy      189 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||
Db      61 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

Qy      249 ACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTGGCGGCCCCG 308
          |||
Db      120 ACTGGACAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTGGCGGCCCCG 179

Qy      309 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
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Db      180 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 428
          |||
Db      240 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429 GCGGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||
Db      300 GCGGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489 GGCAGGCCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 548
          |||
Db      359 GGCAGGCCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 608
          |||
Db      419 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 478

Qy      609 GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479 GTCCACGCTCGCCCGGCTCGTCCGACGCG 507
    
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RESULT 10

AR065267

LOCUS AR065267 736 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5849514.

ACCESSION AR065267

VERSION AR065267.1 GI:5995483

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 736)

AUTHORS Amaral,M.Catherine. and Chen,J.-L.

TITLE Method of identifying agents that modulate UCP2 promoter activity

JOURNAL Patent: US 5849514-A 1 15-DEC-1998;

FEATURES Location/Qualifiers

source 1. .736
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 76.1%; Score 485; DB 2; Length 736;
 Best Local Similarity 99.6%; Pred. No. 2.5e-126;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy      129 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 188
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Qy      189 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||
Db       61 ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

Qy      249 ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 308
          |||
Db      120 ACTGGACAAGACTTGTTTCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCG 179

Qy      309 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
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Db      180 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAGAAAGTCATGGAGAGAACCCTA 428
          |||
Db      240 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGAGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||
Db      300 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489 GGCAGGCCCCGGCCCCGCCCGCAGGCCCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCG 548
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Db      359 GGCAGGCCCCGGCCCCGCCCGCAGGCCCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 608
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Db      419 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACT 478

Qy      609 GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479 GTCCACGCTCGCCCGGCTCGTCCGACGCG 507
  
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RESULT 11

BD061651

LOCUS BD061651 736 bp DNA linear PAT 27-AUG-2002

DEFINITION Regulators of UCP2 gene expression.

ACCESSION BD061651

VERSION BD061651.1 GI:22607256

KEYWORDS JP 2001507943-A/1.

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 736)

AUTHORS Amaral, C.M. and Chen, J.L.

TITLE Regulators of UCP2 gene expression

JOURNAL Patent: JP 2001507943-A 1 19-JUN-2001;
 TULARIK INC

COMMENT PN JP 2001507943-A/1
 PD 19-JUN-2001
 PF 22-APR-1998 JP 1998547120
 PR 25-APR-1997 US 08/846012
 PI CATHERINE M AMARAL, JIN LONG CHEN
 PC C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68 CC
 Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers.

FEATURES Location/Qualifiers
 source 1. .736
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 76.1%; Score 485; DB 2; Length 736;
 Best Local Similarity 99.6%; Pred. No. 2.5e-126;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy      129 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 188
          |||
Db      1 GGGTGGGTAGTTTGGCCAGCGTAGGGGGGCTGGGCCCATAAAAGAGGAAGTGCACCTTAAG 60

Qy      189 ACACGGCCCCGCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 248
          |||
Db      61 ACACGGCCCCGCTGGACGC-TGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTG 119

Qy      249 ACTGGACAAGACTTGTTTCTGGCGGTCACTCTGCCATCCTCACAGAGGTTGGCGGCCCCG 308
          |||
Db      120 ACTGGACAAGACTTGTTTCTGGCGGTCACTCTGCCATCCTCACAGAGGTTGGCGGCCCCG 179

Qy      309 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 368
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Db      180 AGAGAGTGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGA 239

Qy      369 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 428
          |||
Db      240 GTAAACGCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTA 299

Qy      429 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCT 488
          |||
Db      300 GGCGGGGCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAG-T 358

Qy      489 GGCAGGCCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 548
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Db      359 GGCAGGCCCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCGCCCCGAGGCTTAAGCCG 418

Qy      549 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGGGATTGACT 608
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Db      419 CGCCGCCGCCTGCGCGGAGCCCCACTGCGAAGCCAGCTGCGCGCGCCTTGGGATTGACT 478

Qy      609 GTCCACGCTCGCCCGGCTCGTCCGACGCG 637
          |||
Db      479 GTCCACGCTCGCCCGGCTCGTCCGACGCG 507
  
```

RESULT 12

AF208500

LOCUS AF208500 3301 bp DNA linear PRI 09-JAN-2000
 DEFINITION Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.


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Db      2845 TTTTGCCCCAGCGTTAGGGGGGCTGGGCCCCATAAAAGAGGAAGTGCACCTTAAGACACGG 2904

Qy      195 CCCCCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGA 254
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Db      2905 CCCCCTGGACGCTTGTTAGAAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGA 2964

Qy      255 CAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAG 314
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Db      2965 CAAGACTTGTTCCTGGCGGTCAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCGAGAGAG 3024

Qy      315 TGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAAC 374
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Db      3025 TGTGAGGCAGAGGCGGGGAGTGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAAC 3084

Qy      375 GCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGG 434
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Db      3085 GCGGTGATGGGACGCACGGAACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGG 3144

Qy      435 GCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGG 494
      |||
Db      3145 GCGGTCCCCGCGGAAAGGCGGCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGG 3204

Qy      495 CCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCGCGCCGC 554
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Db      3205 CCCGGCCCCGCCCCGAGGCCCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCGCGCCGC 3264

Qy      555 CGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGC 591
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Db      3265 CGCCTGCGCGGAGCCCCACTGCGAAGCCCAGCTGCGC 3301
    
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RESULT 13

AX346794

LOCUS AX346794 5283 bp DNA linear PAT 01-FEB-2002

DEFINITION Sequence 1865 from Patent WO0200928.

ACCESSION AX346794

VERSION AX346794.1 GI:18494680

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.

TITLE Diagnosis of diseases associated with the immune system

JOURNAL Patent: WO 0200928-A 1865 03-JAN-2002;

Epigenomics AG (DE)

FEATURES Location/Qualifiers

source 1. .5283

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 57.2%; Score 364.2; DB 2; Length 5283;

Best Local Similarity 77.4%; Pred. No. 6.6e-92;

Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

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Qy      95 CCTGCAGGAGCCAGCCGCGCGCTCGCTCGCAGGAGGGTGGGTAGTTTGCCAGCGTAGGG 154
      || ||||| || ||||| ||| ||| ||||| ||||| ||||| |||
Db      62 TTTGTAGGAGTTAGTCGCGCGTTCGTTCTAGGAGGGTGGGTAGTTTGTTTAGCGTA-GG 120

Qy     155 GGGCTGGGCCCATAAAAGAGGAAGTGCACCTAAGACACGGCCCCGCTGGACGCTTGTTAG 214
      ||| ||||| ||||| ||||| ||| ||||| ||| ||| |||||
Db     121 GGGTTGGGTTTATAAAAGAGGAAGTGTATTTAAGATACGGTTTAG--TGGACGTTGTTAG 178

Qy     215 AAACCGTCCTGGCTGGGAAGGCAAGAGGTGTGTGACTGGACAAGACTTGTTTCTGGCGGT 274
      ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db     179 AAATCGTTTTTGGTTGGGAAGGTAAGAGGTGTGTGATTGGATAAGATTTGTTTTTGGCGGT 238

Qy     275 CAGTCTTGCCATCCTCACAGAGGTTGGCGGCCCCGAGAGAGTGTGAGGCAGAGCGGGGAG 334
      ||| ||| ||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db     239 TAGTTTTTGTATTATTTTATAGAGGTTGGCGGTTTCGAGAGAGTGTGAGGTAGAGCGGGGAG 298

Qy     335 TGGCAAGGGAGTGACCATCTCGGGGAACGAAGGAGTAAACGCGGTGATGGGACGCACGGA 394
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Db     299 TGGTAAGGGAGTGATTATTTTCGGGAACGAAGGAGTAAACGCGGTGATGGGACGTACGGA 358

Qy     395 AACGGGAGTGGAGAAAGTCATGGAGAGAACCCTAGGCGGGGCGGTCCCCGCGGAAAGGCG 454
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     359 AACGGGAGTGGAGAAAGTTATGGAGAGAATTTTAGGCGGGGCGGTTCGCGGAAAGGCG 418

Qy     455 GCTGCTCCAGGGTCTCCGCACCCAAGTAGGAGCTGGCAGGCCCGGCCCGCCCCGCGAGGC 514
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Db     419 GTTGTTTTAGGGTTTTTCGTATTTAAGTAGGAGTTGGTAGGTTTCGTTTCGTTTCGTAGGT 478

Qy     515 CCCACCCCGGGCCCCCGCCCCGAGGCTTAAGCCGCGCCCGCCCTGCGCGGAGCCCCACT 574
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Db     479 TTTATTTTCGGGTTTCGTTTTTCGAGGTTTAAGTCGCGTCGTCGTTTGCGCGAGTTTATT 538

Qy     575 GCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTCCGAC 634
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Db     539 GCGAAGTTTAGTTGCGCGCGTTTTTGGGATTGATTGTTTACGTTTCGTTTCGTTTCGAC 598

Qy     635 GCG 637
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Db     599 GCG 601

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RESULT 14
AX346795/c
LOCUS      AX346795              5283 bp    DNA        linear    PAT 01-FEB-2002
DEFINITION Sequence 1866 from Patent WO0200928.
ACCESSION  AX346795
VERSION    AX346795.1  GI:18494681
KEYWORDS   .
SOURCE     synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
  AUTHORS  Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE    Diagnosis of diseases associated with the immune system
  JOURNAL  Patent: WO 0200928-A 1866 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES   Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"

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ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1

AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.

TITLE Methods of testing for bronchial asthma or chronic obstructive
 pulmonary disease

JOURNAL Patent: EP 1394274-A 426 03-MAR-2004;
 Genox Research, Inc. (JP)

FEATURES Location/Qualifiers

source 1. .1646
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 10.5%; Score 67; DB 2; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 630
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 Db 1 CACTGCGAAGCCCAGCTGCGCGCGCCTTGGGATTGACTGTCCACGCTCGCCCGGCTCGTC 60

Qy 631 CGACGCG 637
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 Db 61 CGACGCG 67

Search completed: June 6, 2006, 21:24:48
 Job time : 4061 secs

SCORE 1.3 BuildDate: 12/06/2005
